



SEQUENCE LISTING

GENERAL INFORMATION:

(i) APPLICANT: BROW, MARY ANN D.  
LYAMICHEV, VICTOR I.  
OLIVE, DAVID M.

(ii) TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF PATHOGENS

(iii) NUMBER OF SEQUENCES: 165

(iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: MEDLEN & CARROLL  
(B) STREET: 220 MONTGOMERY STREET, SUITE 2200  
(C) CITY: SAN FRANCISCO  
(D) STATE: CALIFORNIA  
(E) COUNTRY: UNITED STATES OF AMERICA  
(F) ZIP: 94104

(v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US  
(B) FILING DATE:  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: CARROLL, PETER G.  
(B) REGISTRATION NUMBER: 32,837  
(C) REFERENCE/DOCKET NUMBER: FORS-01756

(ix) TELECOMMUNICATION INFORMATION:  
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2506 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAGGGGGA TGCTGCCCTT CTTTGAGCCC AAGGGCCGGG TCCTCCTGGT GGACGGCCAC	60
CACCTGGCCT ACCGCACCTT CCACGCCCTG AAGGGCCTCA CCACCAGCCG GGGGGAGCCG	120
GTGCAGGCCG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTCAAGGA GGACGGGAC	180
GCGGTGATCG TGGTCTTGA CGCCAAGGCC CCCTCCTTCC GCCACGAGGC CTACGGGGG	240
TACAAGGCCG GCCGGGCCCG CACGCCGGAG GACTTTCCCC GGCAACTCGC CCTCATCAAG	300

GAGCTGGTGG ACCTCCTGGG GCTGGCGCGC CTGGAGGTCC CGGGCTACGA GGCGGACGAC	360
GTCCTGGCCA GCCTGGCCAA GAAGGCGGAA AAGGAGGGCT ACGAGGTCCG CATCCTCAC	420
GCCGACAAAG ACCTTTACCA GCTCCTTCC GACCGCATCC ACGTCCTCCA CCCCAGGGGG	480
TACCTCATCA CCCCCGGCTG GCTTTGGGAA AAGTACGGCC TGAGGCCCCGA CCAGTGGGCC	540
GACTACCGGG CCCTGACCGG GGACGAGTCC GACAACCTTC CCGGGGTCAA GGGCATCGGG	600
GAGAAGACGG CGAGGAAGCT TCTGGAGGAG TGGGGGAGCC TGGAAGCCCT CCTCAAGAAC	660
CTGGACCGGC TGAAGCCCGC CATCCGGAG AAGATCCTGG CCCACATGGA CGATCTGAAG	720
CTCTCCTGGG ACCTGGCCAA GGTGCGCACC GACCTGCCCG TGGAGGTGGA CTTGCCAAA	780
AGGCGGGAGC CCGACCGGGA GAGGCTTAGG GCCTTCTGG AGAGGCTTGA GTTGGCAGC	840
CTCCTCCACG AGTTCGGCCT TCTGGAAAGC CCCAAGGCCCG TGGAGGAGGC CCCCTGGCCC	900
CCGCCGGAAG GGGCCTTCGT GGGCTTGTG CTTCCCGCA AGGAGCCCAT GTGGGCCGAT	960
CTTCTGGCCC TGGCCGCCGC CAGGGGGGGC CGGGTCCACC GGGCCCCCGA GCCTTATAAA	1020
GCCCTCAGGG ACCTGAAGGA GGCGCGGGGG CTTCTGCCA AAGACCTGAG CGTTCTGGCC	1080
CTGAGGGAAG GCCTTGGCCT CCCGCCGGC GACGACCCCA TGCTCCTCGC CTACCTCTG	1140
GACCCTTCCA ACACCACCCC CGAGGGGGTG GCCCGCGCT ACGGCGGGGA GTGGACGGAG	1200
GAGGCGGGGG AGCGGCCGC CTTTCCGAG AGGCTCTCG CCAACCTGTG GGGGAGGCTT	1260
GAGGGGGAGG AGAGGCTCCT TTGGCTTAC CGGGAGGTGG AGAGGCCCCCT TTCCGCTGTC	1320
CTGGCCCCACA TGGAGGCCAC GGGGGTGCAC CTGGACGTGG CCTATCTCAG GGCCTTGTCC	1380
CTGGAGGTGG CCGAGGAGAT CGCCCGCCTC GAGGCCGAGG TCTTCCGCCT GGCCGGCAC	1440
CCCTTCAACC TCAACTCCCG GGACCAGCTG GAAAGGGTCC TCTTGACGA GCTAGGGCTT	1500
CCCGCCATCG GCAAGACGGA GAAGACCGGC AAGCGCTCCA CCAGCGCCGC CGTCCTGGAG	1560
GCCCTCCCGC AGGCCCACCC CATCGTGGAG AAGATCCTGC AGTACCGGGA GTCACCAAG	1620
CTGAAGAGCA CCTACATTGA CCCCTTGCCG GACCTCATCC ACCCCAGGAC GGGCCGCCTC	1680
CACACCCGCT TCAACCAGAC GGCCACGGCC ACGGGCAGGC TAAGTAGCTC CGATCCAAC	1740
CTCCAGAACCA TCCCCGTCCG CACCCCGCTT GGGCAGAGGA TCCGCCGGGC CTTCATGCC	1800
GAGGAGGGGT GGCTATTGGT GGCCCTGGAC TATAGCCAGA TAGAGCTCAG GGTGCTGGCC	1860
CACCTCTCCG GCGACCGAGAA CCTGATCCGG GTCTTCCAGG AGGGGGGGGA CATCCACACG	1920
GAGACCGCCA GCTGGATGTT CGCGTCCCC CGGGAGGCCG TGGACCCCT GATGCGCCGG	1980
GCGGCCAAGA CCATCAACTT CGGGGTCCCTC TACGGCATGT CGGCCCACCG CCTCTCCCAG	2040
GAGCTAGCCA TCCCTTACGA GGAGGCCCCAG GCCTTCATTG AGCGCTACTT TCAGAGCTTC	2100
CCCAAGGTGC GGGCCTGGAT TGAGAAGACC CTGGAGGAGG GCAGGAGGCG GGGGTACGTG	2160

GAGACCCTCT	TCGGCCGCCG	CCGCTACGTG	CCAGACCTAG	AGGCCCGGGT	GAAGAGCGTG	2220
CGGGAGGCAG	CCGAGCGCAT	GGCCTTCAAC	ATGCCCGTCC	AGGGCACCGC	CGCCGACCTC	2280
ATGAAGCTGG	CTATGGTGAA	GCTCTTCCCC	AGGCTGGAGG	AAATGGGGGC	CAGGATGCTC	2340
CTTCAGGTCC	ACGACGAGCT	GGTCCTCGAG	GCCCCAAAAG	AGAGGGCGGA	GGCCGTGGCC	2400
CGGCTGGCCA	AGGAGGTCAT	GGAGGGGGTG	TATCCCCTGG	CCGTGCCCT	GGAGGTGGAG	2460
GTGGGGATAG	GGGAGGACTG	GCTCTCCGCC	AAGGAGTGAT	ACCACC		2506

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2496 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGGCGATGC	TTCCCTCTT	TGAGCCAAA	GGCCCGTGC	TCCTGGTGG	CGGCCACCAC	60
CTGGCCTACC	GCACCTTCTT	TGCCCTCAAG	GGCCTCACCA	CCAGCCGGG	CGAACCCGTT	120
CAGGCGGTCT	ACGGCTTCGC	CAAAGCCTC	CTCAAGGCC	TGAAGGAGGA	CGGGGACGTG	180
GTGGTGGTGG	TCTTGACGC	CAAGGCCCC	TCCTCCGCC	ACGAGGCCTA	CGAGGCCTAC	240
AAGGCGGGCC	GGGCCCCCAC	CCCGGAGGAC	TTTCCCCGGC	AGCTGGCCCT	CATCAAGGAG	300
TTGGTGGACC	TCCTAGGCCT	TGTGCGGCTG	GAGGTTCCCG	GCTTGAGGC	GGACGACGTG	360
CTGGCCACCC	TGGCCAAGCG	GGCGGAAAAG	GAGGGGTACG	AGGTGCGCAT	CCTCACTGCC	420
GACCGCGACC	TCTACCAGCT	CCTTCGGAG	CGCATCGCCA	TCCTCCACCC	TGAGGGGTAC	480
CTGATCACCC	CGGCGTGGCT	TTACGAGAAG	TACGGCCTGC	GCCCGGAGCA	GTGGTGGAC	540
TACCGGGCCC	TGGCGGGGGA	CCCCTCGGAT	AACATCCCCG	GGGTGAAGGG	CATCGGGGAG	600
AAGACCGCCC	AGAGGCTCAT	CCGCGAGTGG	GGGAGCCTGG	AAAACCTCTT	CCAGCACCTG	660
GACCAGGTGA	AGCCCTCCTT	GGGGGAGAAG	CTCCAGGCCG	GCATGGAGGC	CCTGGCCCTT	720
TCCCGGAAGC	TTTCCCAGGT	GCACACTGAC	CTGCCCTGG	AGGTGGACTT	CGGGAGGCAG	780
CGCACACCCA	ACCTGGAGGG	TCTGCGGCT	TTTTGGAGC	GGTTGGAGTT	TGGAAGCCTC	840
CTCCACGAGT	TCGGCCTCCT	GGAGGGGCCG	AAGGCCAG	AGGAGGCC	CTGGCCCCCT	900
CCGGAAGGGG	CTTTTTGGG	CTTTCCCTT	TCCCGTCCCG	AGCCCATGTG	GGCCGAGCTT	960
CTGGCCCTGG	CTGGGGCGTG	GGAGGGCGC	CTCCATCGGG	CACAAGACCC	CCTTAGGGGC	1020
CTGAGGGACC	TTAAGGGGGT	GCGGGAAATC	CTGGCCAAGG	ACCTGGCGGT	TTTGGCCCTG	1080
CGGGAGGGCC	TGGACCTCTT	CCCAGAGGAC	GACCCCATGC	TCCTGGCCTA	CCTTCTGGAC	1140

CCCTCCAACA CCACCCCTGA	GGGGGTGGCC CGGGCGTTACG	GGGGGGAGTG GACGGAGGAT	1200
GCGGGGGAGA GGGCCCTCCT	GGCGAGCGC CTCTTCCAGA	CCCTAAAGGA GCGCCTTAAG	1260
GGAGAAGAAC GCCTGCTTG	GCTTTACGAG GAGGTGGAGA	AGCCGCTTTC CCGGGTGTG	1320
GCCCGGATGG AGGCCACGGG	GGTCCGGCTG GACGTGGCCT	ACCTCCAGGC CCTCTCCCTG	1380
GAGGTGGAGG CGGAGGTGCG	CCAGCTGGAG GAGGAGGTCT	TCCGCCTGGC CGGCCACCCC	1440
TTCAACCTCA ACTCCCGCGA	CCAGCTGGAG CGGGTGCTCT	TTGACGAGCT GGGCCTGCCT	1500
GCCATCGGCA AGACGGAGAA	GACGGGGAAA CGCTCCACCA	GCGCTGCCGT GCTGGAGGCC	1560
CTGCGAGAGG CCCACCCAT	CGTGGACCAGC ATCCTGCAGT	ACCGGGAGCT CACCAAGCTC	1620
AAGAACACCT ACATAGACCC	CCTGCCGCC CTGGTCCACC	CCAAGACCGG CGGCTCCAC	1680
ACCCGCTTCA ACCAGACGGC	CACCGCCACG GGCAGGCTT	CCAGCTCCGA CCCAACCTG	1740
CAGAACATCC CCGTGCAC	CCCTCTGGC CAGCGCATCC	GCCGAGCCTT CGTGGCCGAG	1800
GAGGGCTGGG TGCTGGTGGT	CTTGGACTAC AGCCAGATTG	AGCTTCGGGT CCTGGCCCAC	1860
CTCTCCGGGG ACGAGAACCT	GATCCGGGTC TTCAGGAGG	GGAGGGACAT CCACACCCAG	1920
ACCGCCAGCT GGATGTTCGG	CGTTTCCCCC GAAGGGTAG	ACCTCTGAT GCGCCGGGG	1980
GCCAAGACCA TCAACTTCGG	GGTGTCTAC GGCAATGTCCG	CCCACCGCCT CTCCGGGGAG	2040
CTTTCCATCC CCTACGAGGA	GGCGGTGGCC TTCATTGAGC	GCTACTTCCA GAGCTACCCC	2100
AAGGTGCGGG CCTGGATTGA	GGGGACCTC GAGGAGGCC	GCCGGCGGGG GTATGTGGAG	2160
ACCCCTTTCG GCCGCCGGCG	CTATGTGCC GACCTAACG	CCCGGGTGAA GAGCGTGCAC	2220
GAGGCGGCGG AGCGCATGGC	CTTCAACATG CCGGTCCAGG	GCACCGCCGC CGACCTCATG	2280
AAGCTGGCCA TGGTGCAGGCT	TTTCCCCCGG CTTCAGGAAC	TGGGGCGAG GATGCTTTG	2340
CAGGTGCACG ACGAGCTGGT	CCTCGAGGCC CCCAAGGACC	GGGCGGAGAG GGTAGCCGCT	2400
TTGGCCAAGG AGGTCACTGGA	GGGGGTCTGG CCCCTGCAGG	TGCCCCTGGA GGTGGAGGTG	2460
GGCCTGGGGG AGGACTGGCT	CTCCGCCAAG GAGTAG		2496

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2504 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGAGGCCA	TGCTTCCGCT	CTTTGAACCC	AAAGGCCGGG	TCCTCCTGGT	GGACGGCCAC	60
CACCTGGCCT	ACCGCACCTT	CTTCGCCCTG	AAGGGCCTCA	CCACGAGCCG	GGCGAACCG	120
GTGCAGGCCG	TCTACGGCTT	CGCCAAGAGC	CTCCTCAAGG	CCCTGAAGGA	GGACGGGTAC	180
AAGGCCGTCT	TCGTGGTCTT	TGACGCCAAG	GCCCCCTCCT	TCCGCCACGA	GGCCTACGAG	240
GCCTACAAGG	CGGGGAGGGC	CCCGACCCCC	GAGGACTTCC	CCCGGCAGCT	CGCCCTCATC	300
AAGGAGCTGG	TGGACCTCCT	GGGGTTTACC	CGCCTCGAGG	TCCCCGGCTA	CGAGGCAGGAC	360
GACGTTCTCG	CCACCCCTGGC	CAAGAAGGCG	GAAAAGGAGG	GGTACGAGGT	GCGCATCCTC	420
ACCGCCGACC	GCGACCTCTA	CCAACTCGTC	TCCGACCGCG	TCGCCGTCC	CCACCCCGAG	480
GGCCACCTCA	TCACCCCGGA	GTGGCTTGG	GAGAAGTACG	GCCTCAGGCC	GGAGCAGTGG	540
GTGGACTTCC	GCGCCCTCGT	GGGGGACCCC	TCCGACAACC	TCCCCGGGGT	CAAGGGCATC	600
GGGGAGAAGA	CGGCCCTCAA	GCTCCTCAAG	GAGTGGGAA	GCCTGGAAA	CCTCCTCAAG	660
AACCTGGACC	GGGTAAAGCC	AGAAAACGTC	CGGGAGAAGA	TCAAGGCCA	CCTGGAAGAC	720
CTCAGGCTCT	CCTTGGAGCT	CTCCCAGGTG	CGCACCGACC	TCCCCCTGGA	GGTGGACCTC	780
GCCCAGGGC	GGGAGCCCGA	CCGGGAGGGG	CTTAGGGCCT	TCCTGGAGAG	GCTGGAGTTC	840
GGCAGCCTCC	TCCACGAGTT	CGGCCTCCTG	GAGGCCCGCG	CCCCCCTGGA	GGAGGCCCGCC	900
TGGCCCCCGC	CGGAAGGGC	CTTCGTGGC	TTCGTCCTCT	CCCGCCCGA	GCCCATGTGG	960
CGGGAGCTTA	AAGCCCTGGC	CGCCTGCAGG	GACGCCGGG	TGCACCGGGC	AGCAGACCCC	1020
TTGGCGGGGC	TAAAGGACCT	CAAGGAGGTC	CGGGGCCTCC	TCGCCAAGGA	CCTCGCCGTC	1080
TTGGCCTCGA	GGGAGGGGCT	AGACCTCGTG	CCCGGGGACG	ACCCCATGCT	CCTCGCCTAC	1140
CTCCTGGACC	CCTCCAACAC	CACCCCGAG	GGGGTGGCGC	GGCGCTACGG	GGGGGAGTGG	1200
ACGGAGGACG	CCGCCAACCG	GGCCCTCCTC	TCGGAGAGGC	TCCATCGGAA	CCTCCTTAAG	1260
CGCCTCGAGG	GGGAGGGAGAA	GCTCCTTGG	CTCTACCGC	AGGTGGAAA	CCCCCTCTCC	1320
CGGGTCCCTGG	CCCACATGGA	GGCCACCGGG	GTACGGCTGG	ACGTGGCCTA	CCTTCAGGCC	1380
CTTTCCCTGG	AGCTTGCAGA	GGAGATCCGC	CGCCTCGAGG	AGGAGGTCTT	CCGCTTGGCG	1440
GGCCACCCCT	TCAACCTCAA	CTCCCAGGAC	CAGCTGGAAA	GGGTGCTCTT	TGACGAGCTT	1500
AGGCTTCCCG	CCTTGGGAA	GACGCAAAG	ACAGGCAAGC	GCTCCACCAAG	CGCCGCCGGTG	1560
CTGGAGGCC	TACGGGAGGC	CCACCCCATC	GTGGAGAAGA	TCCTCCAGCA	CGGGGAGCTC	1620
ACCAAGCTCA	AGAACACCTA	CGTGGACCCC	CTCCCAAGCC	TCGTCCACCC	GAGGACGGGC	1680
CGCCTCCACA	CCCGCTTCAA	CCAGACGGCC	ACGGCCACGG	GGAGGCTTAG	TAGCTCCGAC	1740
CCCAACCTGC	AGAACATCCC	CGTCCGCACC	CCCTTGGCC	AGAGGATCCG	CGGGGCCTTC	1800

GTGGCCGAGG CGGGTTGGGC GTTGGTGGCC CTGGACTATA GCCAGATAGA GCTCCGCGTC	1860
CTCGCCCACC TCTCCGGGGA CGAAAACCTG ATCAGGGTCT TCCAGGAGGG GAAGGACATC	1920
CACACCCAGA CCGCAAGCTG GATGTTCGGC GTCCCCCGG AGGCCGTGGA CCCCCTGATG	1980
CGCCGGGCGG CCAAGACGGT GAACTTCGGC GTCCTCTACG GCATGTCCGC CCATAGGCTC	2040
TCCCAGGAGC TTGCCATCCC CTACGAGGAG GCGGTGGCCT TTATAGAGGC TACTTCCAAA	2100
GCTTCCCCAA GGTGCGGGCC TGGATAGAAA AGACCCCTGGA GGAGGGGAGG AAGCAGGGCT	2160
ACGTGGAAAC CCTCTTCGGA AGAAGGCCT ACCTGCCCCGA CCTCAACGCC CGGGTGAAGA	2220
GCGTCAGGGA GGCGCGGAG CGCATGGCCT TCAACATGCC CGTCCAGGGC ACCGCCGCCG	2280
ACCTCATGAA GCTCGCCATG GTGAAGCTCT TCCCCCGCCT CCGGGAGATG GGGGCCGCA	2340
TGCTCCTCCA GGTCCACGAC GAGCTCCTCC TGGAGGCCCG CCAAGCGCGG GCCGAGGAGG	2400
TGGCGGCTTT GGCCAAGGAG GCCATGGAGA AGGCCTATCC CCTCGCCGTG CCCCTGGAGG	2460
TGGAGGTGGG GATGGGGGAG GACTGGCTTT CCGCCAAGGG TTAG	2504

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu	
1 5 10 15	
Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly	
20 25 30	
Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala	
35 40 45	
Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val	
50 55 60	
Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly	
65 70 75 80	
Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu	
85 90 95	
Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu	
100 105 110	
Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys	
115 120 125	
Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp	
130 135 140	

Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly  
 145 150 155 160  
 Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro  
 165 170 175  
 Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn  
 180 185 190  
 Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu  
 195 200 205  
 Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu  
 210 215 220  
 Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys  
 225 230 235 240  
 Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val  
 245 250 255  
 Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe  
 260 265 270  
 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu  
 275 280 285  
 Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly  
 290 295 300  
 Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp  
 305 310 315 320  
 Leu Leu Ala Leu Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro  
 325 330 335  
 Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu  
 340 345 350  
 Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro  
 355 360 365  
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn  
 370 375 380  
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu  
 385 390 395 400  
 Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu  
 405 410 415  
 Trp Gly Arg Leu Glu Gly Glu Arg Leu Leu Trp Leu Tyr Arg Glu  
 420 425 430  
 Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr Gly  
 435 440 445  
 Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala  
 450 455 460  
 Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His  
 465 470 475 480

Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp  
 485 490 495  
 Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg  
 500 505 510  
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile  
 515 520 525  
 Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr  
 530 535 540  
 Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu  
 545 550 555 560  
 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser  
 565 570 575  
 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln  
 580 585 590  
 Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala  
 595 600 605  
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly  
 610 615 620  
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr  
 625 630 635 640  
 Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro  
 645 650 655  
 Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly  
 660 665 670  
 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu  
 675 680 685  
 Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg  
 690 695 700  
 Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val  
 705 710 715 720  
 Glu Thr Leu Phe Gly Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg  
 725 730 735  
 Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro  
 740 745 750  
 Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu  
 755 760 765  
 Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His  
 770 775 780

Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala  
785 790 795 800

Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro  
805 810 815

Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu  
820 825 830

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 831 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val  
1 5 10 15

Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu  
20 25 30

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys  
35 40 45

Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Val Val Val Val Val  
50 55 60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu Ala Tyr  
65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala  
85 90 95

Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Val Arg Leu Glu Val  
100 105 110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Arg Ala  
115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu  
130 135 140

Tyr Gln Leu Leu Ser Glu Arg Ile Ala Ile Leu His Pro Glu Gly Tyr  
145 150 155 160

Leu Ile Thr Pro Ala Trp Leu Tyr Glu Lys Tyr Gly Leu Arg Pro Glu  
165 170 175

Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile  
180 185 190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Gln Arg Leu Ile Arg  
195 200 205

Glu Trp Gly Ser Leu Glu Asn Leu Phe Gln His Leu Asp Gln Val Lys  
210 215 220

Pro Ser Leu Arg Glu Lys Leu Gln Ala Gly Met Glu Ala Leu Ala Leu  
 225 230 235 240  
 Ser Arg Lys Leu Ser Gln Val His Thr Asp Leu Pro Leu Glu Val Asp  
 245 250 255  
 Phe Gly Arg Arg Arg Thr Pro Asn Leu Glu Gly Leu Arg Ala Phe Leu  
 260 265 270  
 Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu  
 275 280 285  
 Gly Pro Lys Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala  
 290 295 300  
 Phe Leu Gly Phe Ser Phe Ser Arg Pro Glu Pro Met Trp Ala Glu Leu  
 305 310 315 320  
 Leu Ala Leu Ala Gly Ala Trp Glu Gly Arg Leu His Arg Ala Gln Asp  
 325 330 335  
 Pro Leu Arg Gly Leu Arg Asp Leu Lys Gly Val Arg Gly Ile Leu Ala  
 340 345 350  
 Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Leu Asp Leu Phe Pro  
 355 360 365  
 Glu Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr  
 370 375 380  
 Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Glu Trp Thr Glu Asp  
 385 390 395 400  
 Ala Gly Glu Arg Ala Leu Leu Ala Glu Arg Leu Phe Gln Thr Leu Lys  
 405 410 415  
 Glu Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu Glu Val  
 420 425 430  
 Glu Lys Pro Leu Ser Arg Val Leu Ala Arg Met Glu Ala Thr Gly Val  
 435 440 445  
 Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Val Glu Ala  
 450 455 460  
 Glu Val Arg Gln Leu Glu Glu Val Phe Arg Leu Ala Gly His Pro  
 465 470 475 480  
 Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu  
 485 490 495  
 Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser  
 500 505 510  
 Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val  
 515 520 525  
 Asp Arg Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr  
 530 535 540  
 Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Gly Arg Leu His  
 545 550 555 560

Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser  
 565 570 575  
 Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg  
 580 585 590  
 Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Val Leu Val Val Leu  
 595 600 605  
 Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp  
 610 615 620  
 Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Gln  
 625 630 635 640  
 Thr Ala Ser Trp Met Phe Gly Val Ser Pro Glu Gly Val Asp Pro Leu  
 645 650 655  
 Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met  
 660 665 670  
 Ser Ala His Arg Leu Ser Gly Glu Leu Ser Ile Pro Tyr Glu Glu Ala  
 675 680 685  
 Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val Arg Ala  
 690 695 700  
 Trp Ile Glu Gly Thr Leu Glu Glu Gly Arg Arg Gly Tyr Val Glu  
 705 710 715 720  
 Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val  
 725 730 735  
 Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val  
 740 745 750  
 Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Arg Leu Phe  
 755 760 765  
 Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val His Asp  
 770 775 780  
 Glu Leu Val Leu Glu Ala Pro Lys Asp Arg Ala Glu Arg Val Ala Ala  
 785 790 795 800  
 Leu Ala Lys Glu Val Met Glu Gly Val Trp Pro Leu Gln Val Pro Leu  
 805 810 815  
 Glu Val Glu Val Gly Leu Gly Glu Asp Trp Leu Ser Ala Lys Glu  
 820 825 830

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 834 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu  
1 5 10 15

Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly  
20 25 30

Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala  
35 40 45

Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala Val Phe  
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu  
65 70 75 80

Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu  
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys  
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg  
130 135 140

Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His Pro Glu  
145 150 155 160

Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
165 170 175

Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro Ser Asp  
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys Leu  
195 200 205

Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg  
210 215 220

Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu Glu Asp  
225 230 235 240

Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu Pro Leu  
245 250 255

Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly Leu Arg  
260 265 270

Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly  
275 280 285

Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro Pro Pro  
290 295 300

Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp  
305 310 315 320

Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Asp Gly Arg Val His Arg  
 325 330 335  
 Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly  
 340 345 350  
 Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp  
 355 360 365  
 Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro  
 370 375 380  
 Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp  
 385 390 395 400  
 Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg  
 405 410 415  
 Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr  
 420 425 430  
 His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala  
 435 440 445  
 Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu  
 450 455 460  
 Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala  
 465 470 475 480  
 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu  
 485 490 495  
 Phe Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys Thr Gly  
 500 505 510  
 Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His  
 515 520 525  
 Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys  
 530 535 540  
 Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly  
 545 550 555 560  
 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu  
 565 570 575  
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu  
 580 585 590  
 Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu  
 595 600 605  
 Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu  
 610 615 620  
 Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile  
 625 630 635 640  
 His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val  
 645 650 655

Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu  
 660 665 670  
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr  
 675 680 685  
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys  
 690 695 700  
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly  
 705 710 715 720  
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Tyr Val Pro Asp Leu Asn  
 725 730 735  
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn  
 740 745 750  
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val  
 755 760 765  
 Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln  
 770 775 780  
 Val His Asp Glu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu  
 785 790 795 800  
 Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala  
 805 810 815  
 Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala  
 820 825 830  
 Lys Gly

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGNNGGCGA	TGCTTCCCCT	CTTTGAGCCC	AAAGGCCGGG	TCCTCCTGGT	GGACGGCCAC	60
CACCTGGCCT	ACCGCACCTT	CTTCGCCCTG	AAGGGCCTCA	CCACCAGCCG	GGCGGAACCG	120
GTCAGGGCGG	TCTACGGCTT	CGCCAAGAGC	CTCCTCAAGG	CCCTGAAGGA	GGACGGGGAC	180
NNGGCGGTGN	TCGTGGTCTT	TGACGCCAAG	GCCCCCTCCT	TCCGCCACGA	GGCCTACGAG	240
GCCTACAAGG	CGGGCCGGGC	CCCCACCCCG	GAGGACTTTC	CCCGGCAGCT	CGCCCTCATC	300
AAGGAGCTGG	TGGACCTCCT	GGGGCTTGCG	CGCCTCGAGG	TCCCCGGCTA	CGAGGCAGAC	360
GACGTNCTGG	CCACCCCTGGC	CAAGAAGGCG	GAAAAGGAGG	GGTACGAGGT	GCGCATCCTC	420

ACCGCCGACC GCGACCTCTA CCAGCTCCTT TCCGACCGCA TCGCCGTCCT CCACCCCGAG	480
GGGTACCTCA TCACCCCGGC GTGGCTTGG GAGAAGTACG GCCTGAGGCC GGAGCAGTGG	540
GTGGACTACC GGGCCCTGGC GGGGGACCCC TCCGACAACC TCCCCGGGGT CAAGGGCATC	600
GGGGAGAAGA CCGCCCNAGA GCTCCTCNAG GAGTGGGGGA GCCTGGAAAA CCTCCTCAAG	660
AACCTGGACC GGGTGAAGCC CGCCNTCCGG GAGAAGATCC AGGCCCACAT GGANGACCTG	720
ANGCTCTCCT GGGAGCTNTC CCAGGTGCGC ACCGACCTGC CCCTGGAGGT GGACTTCGCC	780
AAGNGGCGGG AGCCCGACCG GGAGGGGCTT AGGGCCTTTC TGGAGAGGCT GGAGTTGGC	840
AGCCTCCTCC ACGAGTCGG CCTCCTGGAG GGCCCCAAGG CCCTGGAGGA GGCCCCCTGG	900
CCCCCGCCGG AAGGGGCTT CGTGGGCTT GTCCCTTCCC GCCCGAGGCC CATGTGGGCC	960
GAGCTCTGG CCCTGGCCGC CGCCAGGGAG GGCGGGTCC ACCGGGCACC AGACCCCTT	1020
ANGGGCCTNA GGGACCTNAAGGAGGTGCGG GGNCTCCTCG CCAAGGACCT GGCGTTTG	1080
GCCCTGAGGG AGGGCCTNGA CCTCNTGCCG GGGGACGACC CCATGCTCCT CGCCTACCTC	1140
CTGGACCCCT CCAACACCAAC CCCCAGGGGG GTGGCCCGGC GCTACGGGGG GGAGTGGACG	1200
GAGGANGCGG GGGAGCGGGC CCTCCTNTCC GAGAGGCTCT TCCNGAACCT NNNGCAGCGC	1260
CTTGAGGGGG AGGAGAGGCT CCTTTGGCTT TACCAGGAGG TGGAGAACCC CCTTTCCCGG	1320
GTCCTGGCCC ACATGGAGGC CACGGGGTN CGGCTGGACG TGGCCTACCT CCAGGCCCTN	1380
TCCCTGGAGG TGGCGGAGGA GATCCGCCGC CTCGAGGAGG AGGTCTTCCG CCTGGCCGGC	1440
CACCCCTTCA ACCTCAACTC CGGGGACCAG CTGGAAAGGG TGCTCTTGA CGAGCTNGGG	1500
CTTCCCGCCA TCGGCAAGAC GGAGAACACN GGCAAGCGCT CCACCAGCGC CGCCGTGCTG	1560
GAGGCCCTNC GNGAGGCCCA CCCCATCGTG GAGAAGATCC TGCAGTACCG GGAGCTCACC	1620
AAGCTCAAGA ACACCTACAT NGACCCCTG CCNGNCCTCG TCCACCCAG GACGGGCCGC	1680
CTCCACACCC GCTTCAACCA GACGGCCACG GCCACGGCA GGCTTAGTAG CTCCGACCCCC	1740
AACCTGCAGA ACATCCCCGT CCGCACCCCN CTGGGCCAGA GGATCCGCCG GGCCTTCGTG	1800
GCCGAGGAGG GNTGGGTGTT GGTGGCCCTG GACTATAGCC AGATAGAGCT CCGGGTCCCTG	1860
GCCCACCTCT CGGGGACGA GAACCTGATC CGGGTCTTCC AGGAGGGAG GGACATCCAC	1920
ACCCAGACCG CCAGCTGGAT GTTCGGCGTC CCCCCGGAGG CGTGGACCC CCTGATGCGC	1980
CGGGCGGCCA AGACCATCAA CTTCGGGTC CTCTACGGCA TGTCCGCCCA CGGCCTCTCC	2040
CAGGAGCTTG CCATCCCCTA CGAGGAGGCG GTGGCCTTCA TTGAGCGCTA CTTCCAGAGC	2100
TTCCCCAAGG TGCGGGCCTG GATTGAGAAG ACCCTGGAGG AGGGCAGGAG GCGGGGGTAC	2160
GTGGAGACCC TCTTCGGCCG CGGGCGCTAC GTGCCGACC TCAACGCCCG GGTGAAGAGC	2220
GTGCGGGAGG CGGCGGAGCG CATGGCCTTC AACATGCCCG TCCAGGGCAC CGCCGCCGAC	2280

CTCATGAAGC TGGCCATGGT GAAGCTCTTC CCCCCGCTNC AGGAAATGGG GGCCAGGATG	2340
CTCCTNCAGG TCCACGACGA GCTGGTCCTC GAGGCCCCA AAGAGCGGGC GGAGGNGGTG	2400
GCCGCTTGG CCAAGGAGGT CATGGAGGGG GTCTATCCCC TGGCCGTGCC CCTGGAGGTG	2460
GAGGTGGGGA TGGGGGAGGA CTGGCTCTCC GCCAAGGAGT AG	2502

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Xaa Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu	
1 5 10 15	
Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly	
20 25 30	
Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala	
35 40 45	
Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Xaa Val	
50 55 60	
Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu Ala	
65 70 75 80	
Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu	
85 90 95	
Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Xaa Arg Leu Glu	
100 105 110	
Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys	
115 120 125	
Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp	
130 135 140	
Leu Tyr Gln Leu Leu Ser Asp Arg Ile Ala Val Leu His Pro Glu Gly	
145 150 155 160	
Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro	
165 170 175	
Glu Gln Trp Val Asp Tyr Arg Ala Leu Xaa Gly Asp Pro Ser Asp Asn	
180 185 190	
Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Xaa Lys Leu Leu	
195 200 205	
Xaa Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg Val	
210 215 220	

Lys Pro Xaa Xaa Arg Glu Lys Ile Xaa Ala His Met Glu Asp Leu Xaa  
 225 230 235 240  
 Leu Ser Xaa Xaa Leu Ser Xaa Val Arg Thr Asp Leu Pro Leu Glu Val  
 245 250 255  
 Asp Phe Ala Xaa Arg Arg Glu Pro Asp Arg Glu Gly Leu Arg Ala Phe  
 260 265 270  
 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu  
 275 280 285  
 Glu Xaa Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly  
 290 295 300  
 Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu  
 305 310 315 320  
 Leu Leu Ala Leu Ala Ala Arg Xaa Gly Arg Val His Arg Ala Xaa  
 325 330 335  
 Asp Pro Leu Xaa Gly Leu Arg Asp Leu Lys Glu Val Arg Gly Leu Leu  
 340 345 350  
 Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Leu Asp Leu Xaa  
 355 360 365  
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn  
 370 375 380  
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu  
 385 390 395 400  
 Asp Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Phe Xaa Asn Leu  
 405 410 415  
 Xaa Xaa Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Xaa Glu  
 420 425 430  
 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly  
 435 440 445  
 Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Val Ala  
 450 455 460  
 Glu Glu Ile Arg Arg Leu Glu Glu Val Phe Arg Leu Ala Gly His  
 465 470 475 480  
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp  
 485 490 495  
 Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg  
 500 505 510  
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile  
 515 520 525  
 Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Asn Thr  
 530 535 540  
 Tyr Ile Asp Pro Leu Pro Xaa Leu Val His Pro Arg Thr Gly Arg Leu  
 545 550 555 560

His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser  
 565 570 575  
 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln  
 580 585 590  
 Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Xaa Leu Val Ala  
 595 600 605  
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly  
 610 615 620  
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr  
 625 630 635 640  
 Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro  
 645 650 655  
 Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly  
 660 665 670  
 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu  
 675 680 685  
 Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg  
 690 695 700  
 Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val  
 705 710 715 720  
 Glu Thr Leu Phe Gly Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg  
 725 730 735  
 Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro  
 740 745 750  
 Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu  
 755 760 765  
 Phe Pro Arg Leu Xaa Glu Met Gly Ala Arg Met Leu Leu Gln Val His  
 770 775 780  
 Asp Glu Leu Val Leu Glu Ala Pro Lys Xaa Arg Ala Glu Xaa Val Ala  
 785 790 795 800  
 Ala Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro  
 805 810 815  
 Leu Glu Val Glu Val Gly Xaa Gly Glu Asp Trp Leu Ser Ala Lys Glu  
 820 825 830  
 Xaa

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1647 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGAATTCCG	GGATGCTGCC	CCTCTTGAG	CCCAAGGGCC	GGGTCTCCT	GGTGGACGGC	60
CACCACTGG	CCTACCGCAC	CTTCCACGCC	CTGAAGGGCC	TCACCACCA	CCGGGGGGAG	120
CCGGTGCAGG	CGGTCTACGG	CTTCGCCAAG	AGCCTCCTCA	AGGCCCTCAA	GGAGGACGGG	180
GACGCGGTGA	TCGTGGTCTT	TGACGCCAAG	GCCCCCTCCT	TCCGCCACGA	GGCCTACGGG	240
GGGTACAAGG	CGGGCCGGGC	CCCCACGCCG	GAGGACTTTC	CCCGGCAACT	CGCCCTCATC	300
AAGGAGCTGG	TGGACCTCCT	GGGGCTGGCG	CGCCTCGAGG	TCCCAGGCTA	CGAGGCGGAC	360
GACGTCTGG	CCAGCCTGGC	CAAGAAGGCG	GAAAAGGAGG	GCTACGAGGT	CCGCATCCTC	420
ACCGCCGACA	AAGACCTTA	CCAGCTCCTT	TCCGACCGCA	TCCACGTCT	CCACCCCGAG	480
GGGTACCTCA	TCACCCCGGC	CTGGCTTTGG	GAAAAGTACG	GCCTGAGGCC	CGACCAGTGG	540
GCCGACTACC	GGGCCCTGAC	CGGGGACGAG	TCCGACAACC	TTCCCGGGGT	CAAGGGCATC	600
GGGGAGAAGA	CGGCGAGGAA	GCTTCTGGAG	GAGTGGGGGA	GCCTGGAAGC	CCTCCTCAAG	660
AACCTGGACC	GGCTGAAGCC	CGCCATCCGG	GAGAAGATCC	TGGCCCACAT	GGACGATCTG	720
AAGCTCTCCT	GGGACCTGGC	CAAGGTGCCG	ACCGACCTGC	CCCTGGAGGT	GGACTTCGCC	780
AAAAGGCGGG	AGCCCGACCG	GGAGAGGCTT	AGGGCCTTTC	TGGAGAGGCT	TGAGTTGGC	840
AGCCTCCTCC	ACGAGTTCGG	CCTTCTGGAA	AGCCCCAAGG	CCCTGGAGGA	GGCCCCCTGG	900
CCCCCGCCGG	AAGGGGCCTT	CGTGGGCTTT	GTGCTTCCC	GCAAGGAGCC	CATGTGGGCC	960
GATCTTCTGG	CCCTGGCCGC	CGCCAGGGGG	GGCCGGGTCC	ACCGGGCCCC	CGAGCCTTAT	1020
AAAGCCCTCA	GGGACCTGAA	GGAGGCGCGG	GGGCTTCTCG	CCAAAGACCT	GAGCGTTCTG	1080
GCCCTGAGGG	AAGGCCTTGG	CCTCCCGCCC	GGCGACGACC	CCATGCTCCT	CGCCTACCTC	1140
CTGGACCCTT	CCAACACCAC	CCCCGAGGGG	GTGGCCGGC	GCTACGGCGG	GGAGTGGACG	1200
GAGGAGGCGG	GGGAGCGGGC	CGCCCTTTC	GAGAGGCTCT	TCGCCAACCT	GTGGGGGAGG	1260
CTTGAGGGGG	AGGAGAGGCT	CCTTGGCTT	TACCGGGAGG	TGGAGAGGCC	CCTTCCGCT	1320
GTCCTGGCCC	ACATGGAGGC	CACGGGGGTG	CGCCTGGACG	TGGCCTATCT	CAGGGCCTTG	1380
TCCCTGGAGG	TGGCCGGGGA	GATCGCCCGC	CTCGAGGCCG	AGGTCTTCCG	CCTGGCCGGC	1440
CACCCCTTCA	ACCTCAACTC	CCGGGACCAG	CTGGAAAGGG	TCCTCTTGA	CGAGCTAGGG	1500

CTTCCCCCCA	TCGGCAAGAC	GGAGAAGACC	GGCAAGCGCT	CCACCAGCGC	CGCCGTCTG	1560
GAGGCCCTCC	GCGAGGCCA	CCCCATCGT	GAGAAGATCC	TGCAGGCATG	CAAGCTTGGC	1620
ACTGGCCGTC	GT	TTTACAAC	GT	CGTGA		1647

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2088 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATGAATTCTGG	GGATGCTGCC	CCTCTTGAG	CCCAAGGGCC	GGGTCTCCT	GGTGGACGGC	60
CACCACTCTGG	CCTACCGCAC	CTTCCACGCC	CTGAAGGGCC	TCACCACCAAG	CCGGGGGGAG	120
CCGGTGCAGG	CGGTCTACGG	CTTCGCCAAG	AGCCTCCTCA	AGGCCCTCAA	GGAGGGACGGG	180
GACGCGGTGA	TCGTGGTCTT	TGACGCCAAG	GCCCCCTCCT	TCCGCCACGA	GGCCTACGGG	240
GGGTACAAGG	CGGGCCGGGC	CCCCACGCCG	GAGGACTTTC	CCCGGCAACT	CGCCCTCATC	300
AAGGAGCTGG	TGGACCTCCT	GGGGCTGGCG	CGCCTCGAGG	TCCCAGGCTA	CGAGGCGGAC	360
GACGTCTCTGG	CCAGCCTGGC	CAAGAAGGGC	GAAAAGGAGG	GCTACGAGGT	CCGCATCCTC	420
ACCGCCGACA	AAGACCTTTA	CCAGCTCCTT	TCCGACCGCA	TCCACGTCT	CCACCCCGAG	480
GGGTACCTCA	TCACCCCGGC	CTGGCTTGG	GAAAAGTACG	GCCTGAGGCC	CGACCAGTGG	540
GCCGACTACC	GGGCCCTGAC	CGGGGACGAG	TCCGACAACC	TTCCCGGGGT	CAAGGGCATC	600
GGGGAGAAGA	CGGCGAGGAA	GCTTCTGGAG	GAGTGGGGGA	GCCTGGAAGC	CCTCCTCAAG	660
AACCTGGACC	GGCTGAAGCC	CGCCATCCGG	GAGAAGATCC	TGGCCCACAT	GGACGATCTG	720
AAGCTCTCCT	GGGACCTGGC	CAAGGTGCGC	ACCGACCTGC	CCCTGGAGGT	GGACTTCGCC	780
AAAAGGCAGG	AGCCCGACCG	GGAGAGGGCTT	AGGGCTTTC	TGGAGAGGCT	TGAGTTGGC	840
AGCCTCCTCC	ACGAGTTCGG	CTTCTGGAA	AGCCCCAAGG	CCCTGGAGGA	GGCCCCCTGG	900
CCCCCGCCGG	AAGGGCCTT	CGTGGCTTT	GTGCTTCCC	GCAAGGAGCC	CATGTGGGCC	960
GATCTTCTGG	CCCTGGCCGC	CGCCAGGGGG	GGCCGGGTCC	ACCGGGCCCC	CGAGCCTTAT	1020
AAAGCCCTCA	GGGACCTGAA	GGAGGGCGGG	GGGCTTCTCG	CCAAAGACCT	GAGCGTTCTG	1080
GCCCTGAGGG	AAGGCCTTGG	CCTCCCGCCC	GGCGACGACC	CCATGCTCCT	CGCCTACCTC	1140
CTGGACCCCTT	CCAACACCAAC	CCCCGAGGGG	GTGGCCCGGC	GCTACGGCGG	GGAGTGGACG	1200
GAGGAGGGCGG	GGGAGCGGGC	CGCCCTTTC	GAGAGGCTCT	TCGCCAACCT	GTGGGGGAGG	1260
CTTGAGGGGG	AGGAGAGGCT	CCTTGGCTT	TACCGGGAGG	TGGAGAGGCC	CCTTCCGCT	1320

GTCCCTGGCCC ACATGGAGGC CACGGGGGTG CGCCTGGACG TGGCCTATCT CAGGGCCTTG	1380
TCCCTGGAGG TGGCCGGGA GATCGCCCGC CTCGAGGCCG AGGTCTTCCG CCTGGCCGGC	1440
CACCCCTTCA ACCTCAACTC CCGGGACCAG CTGGAAAGGG TCCTTTGA CGAGCTAGGG	1500
CTTCCCAGCA TCGGCAAGAC GGAGAAGACC GGCAAGCGCT CCACCAGCGC CGCCGTCCTG	1560
GAGGCCCTCC GCGAGGCCA CCCCATCGTG GAGAAGATCC TGCAAGTACCG GGAGCTCACC	1620
AAGCTGAAGA GCACCTACAT TGACCCCTTG CCGGACCTCA TCCACCCAG GACGGCCGC	1680
CTCCACACCC GCTTCAACCA GACGGCCACG GCCACGGCA GGCTAAGTAG CTCCGATCCC	1740
AACCTCCAGA ACATCCCCGT CCGCACCCCG CTTGGCAGA GGATCCGCCG GGCCCTTCATC	1800
GCCGAGGAGG GGTGGCTATT GGTGGCCCTG GACTATAGCC AGATAGAGCT CAGGGTGCTG	1860
GCCCACCTCT CCGGCGACGA GAACCTGATC CGGGTCTTCC AGGAGGGCG GGACATCCAC	1920
ACGGAGACCG CCAGCTGGAT GTTCGGCGTC CCCCAGGAGG CCGTGGACCC CCTGATGCGC	1980
CGGGCGGCCA AGACCATCAA CTTCGGGGTC CTCTACGGCA TGTCGGCCCA CCGCCTCTCC	2040
CAGGAGCTAG CTAGCCATCC CTTACGAGGA GGCCCAGGCC TTCATTGA	2088

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 962 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGAATTCTGG GGATGCTGCC CCTCTTGAG CCCAAGGGCC GGGTCCTCCT GGTGGACGGC	60
CACCAACCTGG CCTACCGCAC CTTCCACGCC CTGAAGGGCC TCACCACCAAG CGGGGGGGAG	120
CCGGTGCAGG CGGTCTACGG CTTCGCCAAG AGCCTCCTCA AGGCCCTCAA GGAGGACGGG	180
GACGCGGTGA TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGGG	240
GGGTACAAGG CGGGCCGGGC CCCCACGCCG GAGGACTTTC CCCGGCAACT CGCCCTCATC	300
AAGGAGCTGG TGGACCTCCT GGGGCTGGCG CGCCTCGAGG TCCCAGGCTA CGAGGCGGAC	360
GACGTCTGG CCAGCCTGGC CAAGAAGGCG GAAAAGGAGG GCTACGAGGT CCGCATTCTC	420
ACCGCCGACA AAGACCTTTA CCAGCTTCTT TCCGACCGCA TCCACGTCTT CCACCCCGAG	480
GGGTACCTCA TCACCCCGGC CTGGCTTGG GAAAAGTACG GCCTGAGGCC CGACCAAGTGG	540
GCCGACTACC GGGCCCTGAC CGGGGACGAG TCCGACAACC TTCCCGGGGT CAAGGGCATC	600
GGGGAGAAGA CGGCGAGGAA GCTTCTGGAG GAGTGGGGGA GCCTGGAAGC CCTCCTCAAG	660
AACCTGGACC GGCTGAAGCC CGCCATCCGG GAGAAGATCC TGGCCCACAT GGACGATCTG	720

AAGCTCTCCT	GGGACCTGGC	CAAGGTGCGC	ACCGACCTGC	CCCTGGAGGT	GGACTTCGCC	780
AAAAGGCGGG	AGCCCGACCG	GGAGAGGCTT	AGGGCCTTTC	TGGAGAGGCT	TGAGTTGGC	840
AGCCTCCTCC	ACGAGTTCGG	CCTTCTGGAA	AGCCCCAAGT	CATGGAGGGG	GTGTATCCCC	900
TGGCCGTGCC	CCTGGAGGTG	GAGGTGGGGA	TAGGGGAGGA	CTGGCTCTCC	GCCAAGGAGT	960
GA						962

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1600 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGGAATTCTG	GGGATGCTGC	CCCTCTTGA	GCCCAAGGGC	CGGGTCCTCC	TGGTGGACGG	60
CCACCACCTG	GCCTACCGCA	CCTTCCACGC	CCTGAAGGGC	CTCACCAACCA	GCCGGGGGGA	120
GCCGGTGCAG	GCGGTCTACG	GCTTCGCCAA	GAGCCTCCTC	AAGGCCCTCA	AGGAGGACGG	180
GGACGCGGTG	ATCGTGGTCT	TTGACGCCAA	GGCCCCCTCC	TTCCGCCACG	AGGCCTACGG	240
GGGGTACAAG	GCAGGCCGGG	CCCCCACGCC	GGAGGACTTT	CCCCGGCAAC	TCGCCCTCAT	300
CAAGGAGCTG	GTGGACCTCC	TGGGGCTGGC	GCGCCTCGAG	GTCCCGGGCT	ACGAGGCGGA	360
CGACGTCTG	GCCAGCCTGG	CCAAGAAGGC	GGAAAAGGAG	GGCTACGAGG	TCCGCATCCT	420
CACCGCCGAC	AAAGACCTTT	ACCAGCTCCT	TTCCGACCGC	ATCCACGTCC	TCCACCCCGA	480
GGGGTACCTC	ATCACCCCGG	CCTGGCTTTG	GGAAAAGTAC	GGCCTGAGGC	CCGACCAGTG	540
GGCCGACTAC	CGGGCCCTGA	CCGGGGACGA	GTCCGACAAC	CTTCCCAGGG	TCAAGGGCAT	600
CGGGGAGAAG	ACGGCGAGGA	AGCTTCTGGA	GGAGTGGGGG	AGCCTGGAAG	CCCTCCTCAA	660
GAACCTGGAC	CGGCTGAAGC	CCGCCATCCG	GGAGAAAGTC	CTGGCCACACA	TGGACGATCT	720
GAAGCTCTCC	TGGGACCTGG	CCAAGGTGCG	CACCGACCTG	CCCCTGGAGG	TGGACTTCGC	780
CAAAGGCGG	GAGCCCGACC	GGGAGAGGCT	TAGGGCCTTT	CTGGAGAGGC	TTGAGTTGG	840
CAGCCTCCTC	CACGAGTTCG	GCCTTCTGGA	AAGCCCCAAG	ATCCGCCGGG	CCTTCATCGC	900
CGAGGAGGGG	TGGCTATTGG	TGGCCCTGGA	CTATAGCCAG	ATAGAGCTCA	GGGTGCTGGC	960
CCACCTCTCC	GGCGACGAGA	ACCTGATCCG	GGTCTTCCAG	GAGGGGCGGG	ACATCCACAC	1020
GGAGACCGCC	AGCTGGATGT	TCGGCGTCCC	CCGGGAGGCC	GTGGACCCCC	TGATGCGCCG	1080
GGCGGCCAAG	ACCATCAACT	TCGGGGTCCT	CTACGGCATG	TCGGCCCAACC	GCCTCTCCCA	1140
GGAGCTAGCC	ATCCCTTACG	AGGAGGCCA	GGCCTTCATT	GAGCGCTACT	TTCAGAGCTT	1200

CCCCAAGGTG CGGGCCTGGA TTGAGAAGAC CCTGGAGGAG GGCAGGAGGC GGGGGTACGT	1260
GGAGACCCTC TTCGGCCGCC GCCGCTACGT GCCAGACCTA GAGGCCCGGG TGAAGAGCGT	1320
GCGGGAGGCG GCCGAGCGCA TGGCCTTCAA CATGCCCGTC CGGGGCACCG CGCCGACCT	1380
CATGAAGCTG GCTATGGTGA AGCTCTTCCC CAGGCTGGAG GAAATGGGGG CCAGGATGCT	1440
CCTTCAGGTC CACGACGAGC TGGTCCTCGA GGCCCCAAA GAGAGGGCGG AGGCCGTGGC	1500
CCGGCTGGCC AAGGAGGTCA TGGAGGGGGT GTATCCCTG GCCGTGCCCG TGGAGGTGGA	1560
GGTGGGGATA GGGGAGGACT GGCTCTCCGC CAAGGAGTGA	1600

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CACGAATTCTG GGGATGCTGC CCCTCTTGA GCCCAA	36
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(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTGAGATCTA TCACTCCTTG GCGGAGAGCC AGTC	34
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(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 91 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TAATACGACT CACTATAGGG AGACCGGAAT TCGAGCTCGC CGGGCGAGC TCGAATTCCG	60
TGTATTCTAT AGTGTACCT AAATCGAATT C	91

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TAATACGACT CACTATAGGG

20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAATTCGATT TAGGTGACAC TATAGAA

27

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTAATCATGG TCATAGCTGG TAGCTTGCTA C

31

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGATCCTCTA GAGTCGACCT GCAGGCATGC CTACCTTGTT AG

42

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGATCCTCTA GAGTCGACCT GCAGGCATGC

30

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2502 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATGAATTCCG	GGATGCTGCC	CCTCTTGAG	CCCAAGGGCC	GGGTCTCCT	GGTGGACGGC	60
CACCAACCTGG	CCTACCGCAC	CTTCCACGCC	CTGAAGGGCC	TCACCACCAAG	CCGGGGGGAG	120
CCGGTGCAGG	CGGTCTACGG	CTTCGCCAAG	AGCCTCCTCA	AGGCCCTCAA	GGAGGGACGGG	180
GACGCGGTGA	TCGTGGTCTT	TGACGCCAAG	GCCCCCTCCT	TCCGCCACGA	GGCCTACGGG	240
GGGTACAAGG	CGGGCCGGGC	CCCCACGCCG	GAGGACTTTC	CCCGGCAACT	CGCCCTCATC	300
AAGGAGCTGG	TGGACCTCCT	GGGGCTGGCG	CGCCTCGAGG	TCCCGGGCTA	CGAGGCGGAC	360
GACGTCTGG	CCAGCCTGGC	CAAGAAGGCG	GAAAAGGAGG	GCTACGAGGT	CCGCATCCTC	420
ACCGCCGACA	AAGACCTTTA	CCAGCTCCTT	TCCGACCGCA	TCCACGTCT	CCACCCCGAG	480
GGGTACCTCA	TCACCCCCGGC	CTGGCTTGG	GAAAAGTACG	GCCTGAGGCC	CGACCAGTGG	540
GCCGACTACC	GGGCCCTGAC	CGGGGACGAG	TCCGACAACC	TTCCCGGGGT	CAAGGGCATC	600
GGGGAGAAGA	CGGCGAGGAA	GCTTCTGGAG	GAGTGGGGGA	GCCTGGAAGC	CCTCCTCAAG	660
AACCTGGACC	GGCTGAAGCC	CGCCATCCGG	GAGAAGATCC	TGGCCCACAT	GGACGATCTG	720
AAGCTCTCCT	GGGACCTGGC	CAAGGTGCGC	ACCGACCTGC	CCCTGGAGGT	GGACTTCGCC	780
AAAAGGCGGG	AGCCCGACCG	GGAGAGGGCTT	AGGGCCTTTC	TGGAGAGGCT	TGAGTTGGC	840
AGCCTCCTCC	ACGAGTTCGG	CCTTCTGGAA	AGCCCCAAGG	CCCTGGAGGA	GGCCCCCTGG	900
CCCCCGCCGG	AAGGGGCCTT	CGTGGGCTT	GTGCTTCCCC	GCAAGGAGCC	CATGTGGGCC	960
GATCTTCTGG	CCCTGGCCGC	CGCCAGGGGG	GGCCGGGTCC	ACCGGGCCCC	CGAGCCTTAT	1020
AAAGCCCTCA	GGGACCTGAA	GGAGGCGCGG	GGGCTTCTCG	CCAAAGACCT	GAGCGTTCTG	1080

GCCCTGAGGG AAGGCCTTGG CCTCCCGCCC GGCGACGACC CCATGCTCCT CGCCTACCTC	1140
CTGGACCCTT CCAACACCAAC CCCCAGGGGG GTGGCCCGGC GCTACGGCGG GGAGTGGACG	1200
GAGGAGGGCGG GGGAGCGGGC CGCCCTTCC GAGAGGCTCT TCGCCAACCT GTGGGGGAGG	1260
CTTGAGGGGG AGGAGAGGCT CCTTTGGCTT TACCGGGAGG TGGAGAGGCC CCTTCCGCT	1320
GTCCTGGCCC ACATGGAGGC CACGGGGGTG CGCCTGGACG TGGCCTATCT CAGGGCCTTG	1380
TCCCTGGAGG TGGCCGGGA GATCGCCCGC CTCGAGGCCG AGGTCTTCCG CCTGGCCGGC	1440
CACCCCTTCA ACCTCAACTC CCGGGACCAG CTGGAAAGGG TCCTCTTGA CGAGCTAGGG	1500
CTTCCCGCCA TCGGCAAGAC GGAGAAGACC GGCAAGCGCT CCACCAGCGC CGCCGTCTG	1560
GAGGCCCTCC GCGAGGCCA CCCCATCGTG GAGAAGATCC TGCAGTACCG GGAGCTCACC	1620
AAGCTGAAGA GCACCTACAT TGACCCCTTG CCGGACCTCA TCCACCCAG GACGGGCCGC	1680
CTCCACACCC GCTTCAACCA GACGGCCACG GCCACGGCA GGCTAAGTAG CTCCGATCCC	1740
AACCTCCAGA ACATCCCCGT CCGCACCCCG CTTGGCAGA GGATCCGCCG GGCCTTCATC	1800
GCCGAGGAGG GGTGGCTATT GGTGGCCCTG GACTATAGCC AGATAGAGCT CAGGGTGCTG	1860
GCCCACCTCT CCGGGCACGA GAACCTGATC CGGGTCTTCC AGGAGGGCGG GGACATCCAC	1920
ACGGAGACCG CCAGCTGGAT GTTCGGCGTC CCCCCGGAGG CCGTGGACCC CCTGATGCGC	1980
CGGGCGGCCA AGACCATAA CTTCGGGTC CTCTACGGCA TGTCGGCCCA CCGCCTCTCC	2040
CAGGAGCTAG CCATCCCTTA CGAGGAGGCC CAGGCCCTCA TTGAGCGCTA CTTTCAGAGC	2100
TTCCCCAAGG TGCAGGCCCTG GATTGAGAAG ACCCTGGAGG AGGGCAGGAG GCAGGGGTAC	2160
GTGGAGACCC TCTTCGGCCG CCGCCGCTAC GTGCCAGACC TAGAGGCCCG GGTGAAGAGC	2220
GTGCGGGAGG CGGCCGAGCG CATGGCCTTC AACATGCCCG TCCGGGGCAC CGCCGCCGAC	2280
CTCATGAAGC TGGCTATGGT GAAGCTCTTC CCCAGGCTGG AGGAAATGGG GGCCAGGATG	2340
CTCCTTCAGG TCCACGACGA GCTGGTCCTC GAGGCCCAA AAGAGAGGGC GGAGGCCGTG	2400
GCCCGGCTGG CCAAGGAGGT CATGGAGGGG GTGTATCCCC TGGCCGTGCC CCTGGAGGTG	2460
GAGGTGGGAGA TAGGGGAGGA CTGGCTCTCC GCCAAGGAGT GA	2502

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GATTTAGGTG ACACATATAG

19

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CGGACGAACA AGCGAGACAG CGACACAGGT ACCACATGGT ACAAGAGGCA AGAGAGACGA	60
CACAGCAGAA AC	72

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTTTCTGCTG TGTCGTCTCT CTTGCCTCTT GTACCATGTG GTACCTGTGT CGCTGTCTCG	60
CTTGTTCGTC	70

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GACGAACAAG CGAGACAGCG	20
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(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTTTCTGCTG TGTGCTCTCT CTTG

24

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCTCTTGTAC CATGTGGTAC CTGTGTCGCT GTCTCGCTTG TTTCGTC

46

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ACACAGGTAC CACATGGTAC AAGAGGCAAG AGAGACGACA CAGCAGAAC

50

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Asn Ser  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 969 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATGGCTAGCA TGACTGGTGG ACAGCAAATG GGTGGATCA ATTGGGGAT GCTGCCCTC	60
TTTGAGCCA AGGGCCGGGT CCTCCTGGTG GACGCCACC ACCTGGCCTA CCGCACCTTC	120
CACGCCCTGA AGGGCCTCAC CACCAGCCGG GGGGAGCCGG TGCAGGCCGT CTACGGCTTC	180
GCCAAGAGCC TCCTCAAGGC CCTCAAGGAG GACGGGGACG CGGTGATCGT GGTCTTGAC	240
GCCAAGGCC CCTCCTTCG CCACGAGGCC TACGGGGGT ACAAGGCCGG CGGGGCCCGC	300
ACGCCGGAGG ACTTCCCCG GCAACTCGCC CTCATCAAGG AGCTGGTGGA CCTCCTGGGG	360
CTGGCGGCC TCGAGGTCCC GGGCTACGAG GCGGACGACG TCCTGGCCAG CCTGGCCAAG	420
AAGGCGGAAA AGGAGGGCTA CGAGGTCCGC ATCCTCACCG CCGACAAAGA CCTTACCAAG	480
CTTCTTCCG ACCGCATCCA CGTCCTCAC CCCGAGGGT ACCTCATCAC CCCGGCCTGG	540
CTTGGAAA AGTACGGCCT GAGGCCGAC CAGTGGCCG ACTACCGGGC CCTGACCGGG	600
GACGAGTCG ACAACCTTC CGGGGTCAAG GGCATCGGG AGAAGACGGC GAGGAAGCTT	660
CTGGAGGAGT GGGGAGCCT GGAAGCCCTC CTCAAGAAC TGGACCGGCT GAAGCCGCC	720
ATCCGGGAGA AGATCCTGGC CCACATGGAC GATCTGAAGC TCTCCTGGGA CCTGGCCAAG	780
GTGCGCACCG ACCTGCCCCT GGAGGTGGAC TTGCCAAAA GGCGGGAGCC CGACCGGGAG	840
AGGCTTAGGG CCTTCTGGA GAGGCTTGAG TTTGGCAGCC TCCTCCACGA GTTGGCCTT	900
CTGGAAAGCC CCAAGTCATG GAGGGGTGT ATCCCCTGGC CGTGCCCTG GAGGTGGAGG	960
TGGGGATAG	969

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 948 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGGCTAGCA TGACTGGTGG ACAGCAAATG GGTGGATCA ATTGGGGAT GCTGCCCTC	60
TTTGAGCCA AGGGCCGGGT CCTCCTGGTG GACGCCACC ACCTGGCCTA CCGCACCTTC	120
CACGCCCTGA AGGGCCTCAC CACCAGCCGG GGGGAGCCGG TGCAGGCCGT CTACGGCTTC	180
GCCAAGAGCC TCCTCAAGGC CCTCAAGGAG GACGGGGACG CGGTGATCGT GGTCTTGAC	240
GCCAAGGCC CCTCCTTCG CCACGAGGCC TACGGGGGT ACAAGGCCGG CGGGGCCCGC	300
ACGCCGGAGG ACTTCCCCG GCAACTCGCC CTCATCAAGG AGCTGGTGGA CCTCCTGGGG	360
CTGGCGGCC TCGAGGTCCC GGGCTACGAG GCGGACGACG TCCTGGCCAG CCTGGCCAAG	420

AAGGCGGAAA AGGAGGGCTA CGAGGTCCGC ATCCTCACCG CCGACAAAGA CCTTTACCAG	480
CTTCTTCCG ACCGCATCCA CGTCCTCCAC CCCGAGGGGT ACCTCATCAC CCCGGCCTGG	540
CTTTGGGAAA AGTACGGCCT GAGGCCGCAC CAGTGGCCCG ACTACCGGGC CCTGACCGGG	600
GACGAGTCCG ACAACCTCC CGGGGTCAAG GGCATCGGGG AGAAGACGGC GAGGAAGCTT	660
CTGGAGGAGT GGGGGAGCCT GGAAGCCCTC CTCAAGAACC TGGACCGGCT GAAGCCGCC	720
ATCCGGGAGA AGATCCTGGC CCACATGGAC GATCTGAAGC TCTCCTGGGA CCTGGCCAAG	780
GTGCGCACCG ACCTGCCCT GGAGGTGGAC TTGCGCAAAA GGCGGGAGCC CGACCGGGAG	840
AGGCTTAGGG CCTTTCTGGA GAGGCTTGAG TTTGGCAGCC TCCTCCACGA GTTCGGCCTT	900
CTGGAAAGCC CCAAGGCCGC ACTCGAGCAC CACCACCAAC ACCACTGA	948

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 206 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGCCAGGGTT TTCCCAGTCA CGACGTTGTA AAACGACGGC CAGTGAATTG TAATACGACT	60
CACTATAGGG CGAATTCGAG CTCGGTACCC GGGGATCCTC TAGAGTCGAC CTGCAGGCAT	120
GCAAGCTTGA GTATTCTATA GTGTCACCTA AATAGCTTGG CGTAATCATG GTCATAGCTG	180
TTTCCTGTGT GAAATTGTTA TCCGCT	206

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 43 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TTCTGGGTTTC TCTGCTCTCT GGTCGCTGTC TCGCTTGTTC GTC	43
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(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCTGTCTCGC TTGTTCGTC

19

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GACGAACAAG CGAGACAGCG

20

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TTCTGGGTTC TCTGCTCTCT GGTC

24

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GACGAACAAG CGAGACAGCG ACCAGAGAGC AGAGAACCCA GAA

43

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ACCAGAGAGC AGAGAACCCA GAA

23

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AACAGCTATG ACCATGATT A C

21

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 157 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCGGGAA  
 TCCTACATGG TTCCTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA  
 GATCTGGGCT ATGACTATAG CTATCTACAA GATTAG

60

120

157

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 157 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTAGACA TAACCGGGAA  
 TCCTACATGG TTCCTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA  
 GATCTGGGCT ATGACTATAG CTATCTACAA GATTAG

60

120

157

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CACCGTCCTC TTCAAGAAG

19

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTGAATCTTG TAGATAGCTA

20

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 339 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GCCTTATTTT ACTTTAAAAAA TTTCAAAATG TTTCTTTAT ACACAATATG TTTCTTAGTC	60
TGAATAACCT TTTCCCTCTGC AGTATTTTG AGCAGTGGCT CCGAAGGCAC CGTCCTCTTC	120
AAGAAGTTA TCCAGAAGCC AATGCACCCA TTAGACATAA CCGGGAATCC TACATGGTTC	180
CTTTTATACC ACTGTACAGA AATGGTGATT TCTTTATTC ATCCAAAGAT CTGGGCTATG	240
ACTATAGCTA TCTACAAGAT TCAGGTAAAG TTTACTTCT TTCAGAGGAA TTGCTGAATC	300
TAGTGTTACC AATTATTTT GAGATAACAC AAAACTTA	339

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GCCTTATTTT ACTTTAAAAAA T	21
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(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TAAAGTTTG TGTTATCTCA

20

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCGGGAA

60

TCCTACATGG TTCCTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTAT TTCATCCAAA

120

GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAAG

157

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CTGAATCTTG TAGATAGCTA TAGTCATAGC CCAGATCTT GGATGAAATA AAGAAATCAC

60

CATTCTGTG CAGTGGTATA AAAGGAACCA TGTAGGATTC CCGGTTATGT CCAATGGGTG

120

CATTGGCTTC TGGATAAACT TCTTGAAGAG GACGGTG

157

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AGCGGATAAAC AATTCACAC AGGAAACAGC TATGACCATG ATTACGCCAA GCTATTTAGG

60

TGACACTATA GAATACTCAA GCTTGCATGC CTGCAGGTCG ACTCTAGAGG ATCCCCGGGT

120

ACCGAGCTCG AATTGCCCT ATAGTGAGTC GTATTAGGAT CCGTG

165

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 206 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CGCCAGGGTT TTCCCAGTCA CGACGTTGTA AAACGACGGC CAGTGAATTG TAATACGACT	60
CACTATAGGG CGAATTCGAG CTCGGTACCC GGGGATCCTC TAGAGTCGAC CTGCAGGCAT	120
GCAAGCTTGA GTATTCTATA GTGTCACCTA AATAGCTTGG CGTAATCATG GTCATAGCTG	180
TTTCCTGTGT GAAATTGTTA TCCGCT	206

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

AGCGGATAAC AATTCACAC AGGA	24
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(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CACGGATCCT AATACGACTC ACTATAGGG	29
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(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CGCCAGGGTT TTCCCAGTCA CGAC	24
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(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 157 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTAGACA TAACCGGGAA	60
TCCTACATGG TTCCTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTAT TTCATCCAAA	120
GATCTGGGCT ATGACTATAG CTATCTACAA GATTCA	157

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 157 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCAGGAA	60
TCCTACATGG TTCCTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTAT TTCATCCAAA	120
GATCTGGGCT ATGACTATAG CTATCTACAA GATTCA	157

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 378 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCGGGAA	60
TCCTACATGG TTCCTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTAT TTCATCCAAA	120
GATCTGGGCT ATGACTATAG CTATCTACAA GATTCA GACC CAGACTCTTT TCAAGACTAC	180
ATTAAGTCCT ATTTGGAACA AGCGAGTCGG ATCTGGTCAT GGCTCCTTGG GGCGGCGATG	240
GTAGGGGCCG TCCTCACTGC CCTGCTGGCA GGGCTTGTGA GCTTGCTGTG TCGTCACAAG	300
AGAAAGCAGC TTCCTGAAGA AAAGCAGCCA CTCCTCATGG AGAAAGAGGA TTACCACAGC	360
TTGTATCAGA GCCATTAA	378

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 378 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCAGGAA	60
TCCTACATGG TTCCTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTAT TTCATCCAAA	120
GATCTGGCT ATGACTATAG CTATCTACAA GATTCA GATTCA GACTCTTT TCAAGACTAC	180
ATTAAGTCCT ATTTGGAACA AGCGAGTCGG ATCTGGTCAT GGCTCCTTGG GGCGGCGATG	240
GTAGGGGCCG TCCTCACTGC CCTGCTGGCA GGGCTTGTGA GCTTGCTGTG TCGTCACAAG	300
AGAAAGCAGC TTCTGAAGA AAAGCAGCCA CTCCTCATGG AGAAAGAGGA TTACCA CAGC	360
TTGTATCAGA GCCATTAA	378

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1059 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GCAAGTTGG CTTTGGGCA CAAACTGCA CAGAGAGACG ACTCTGGTG AGAAGAAACA	60
TCTTCGATTG GAGTCCCCA GAGAAGGACA AATTTTGCTACACT TTAGCAAAGC	120
ATACCATCAG CTCAGACTAT GTCATCCCCA TAGGGACCTA TGGCAAATG AAAATGGAT	180
CAACACCCAT GTTAACGAC ATCAATATTT ATGACCTCTT TGTCTGGATG CATTATTATG	240
TGTCAATGGA TGCAGTGCTT GGGGGATATG AAATCTGGAG AGACATTGAT TTTGCCATG	300
AAGCACCAGC TTTCTGCCT TGGCATAGAC TCTTCTTGTG GCGGTGGAA CAAGAAATCC	360
AGAAGCTGAC AGGAGATGAA AACTTCACTA TTCCATATTG GGACTGGCGG GATGCAGAAA	420
AGTGTGACAT TTGCACAGAT GAGTACATGG GAGGTCA GCA CCCACAAAT CCTAACCTAC	480
TCAGCCCCAGC ATCATTCTTC TCCTCTTGGC AGATTGTCTG TAGCCGATTG GAGGAGTACA	540
ACAGCCATCA GTCTTATGC AATGGAACGC CCGAGGGACC TTTACGGCGT AATCCTGGAA	600
ACCATGACAA ATCCAGAACCC CCAAGGCTCC CCTCTTCAGC TGATGTAGAA TTTGCCTGA	660
GTGGACCCA ATATGAATCT GGTTCCATGG ATAAAGCTGC CAATTCAGC TTTAGAAATA	720

CACTGGAAAGG ATTTGCTAGT CCACCTTACTG GGATAGCGGA TGCCTCTCAA AGCAGCATGC	780
ACAATGCCTT GCACATCTAT ATGAATGGAA CAATGTCCCA GGTACAGGGAA TCTGCCAACG	840
ATCCTATCTT CCTTCTTCAC CATGCATTG TTGACAGTAT TTTTGAGCAG TGGCTCCGAA	900
GGCACCGTCC TCTTCAAGAA GTTTATCCAG AAGCCAATGC ACCCATTGGA CATAACCAGGG	960
AATCCTACAT GGTTCCCTTT ATACCACTGT ACAGAAATGG TGATTTCTTT ATTCATCCA	1020
AAGATCTGGG CTATGACTAT AGCTATCTAC AAGATTCA	1059

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1059 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GCAAGTTGG CTTTGGGGA CCAAACGTCA CAGAGAGACG ACTCTGGTG AGAAGAAACA	60
TCTTCGATT GAGTGCCCA GAGAAGGACA AATTCTTGC CTACCTCACT TTAGCAAAGC	120
ATACCATCAG CTCAGACTAT GTCATCCCA TAGGGACCTA TGGCAAATG AAAATGGAT	180
CAACACCCAT GTTAAACGAC ATCAATATTG ATGACCTCTT TGTCTGGATG CATTATTATG	240
TGTCAATGGA TGCACTGCTT GGGGGATATG AAATCTGGAG AGACATTGAT TTTGCCATG	300
AAGCACCAGC TTTCTGCCT TGGCATAGAC TCTCTTGTT GCGGTGGAA CAAGAAATCC	360
AGAAGCTGAC AGGAGATGAA AACTTCACTA TTCCATATTG GGACTGGCGG GATGCAGAAA	420
AGTGTGACAT TTGCACAGAT GAGTACATGG GAGGTCAAGCA CCCCACAAAT CCTAACTTAC	480
TCAGCCCAGC ATCATTCTTC TCCTCTTGGC AGATTGTCTG TAGCCGATTG GAGGAGTACA	540
ACAGCCATCA GTCTTATGC AATGGAACGC CCGAGGGACC TTTACGGCGT AATCCTGGAA	600
ACCATGACAA ATCCAGAACCC CCAAGGCTCC CCTCTTCAGC TGATGTAGAA TTTTGCTGA	660
GTGGACCCA ATATGAATCT GGTTCCATGG ATAAAGCTGC CAATTCAGC TTTAGAAATA	720
CACTGGAAAGG ATTTGCTAGT CCACTTACTG GGATAGCGGA TGCCTCTCAA AGCAGCATGC	780
ACAATGCCTT GCACATCTAT ATGAATGGAA CAATGTCCCA GGTACAGGGAA TCTGCCAACG	840
ATCCTATCTT CCTTCTTCAC CATGCATTG TTGACAGTAT TTTTGAGCAG TGGCTCCGAA	900
GGCACCGTCC TCTTCAAGAA GTTTATCCAG AAGCCAATGC ACCCATTGGA CATAACCAGG	960
AATCCTACAT GGTTCCCTTT ATACCACTGT ACAGAAATGG TGATTTCTTT ATTCATCCA	1020
AAGATCTGGG CTATGACTAT AGCTATCTAC AAGATTCA	1059

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1587 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ATGCTCCTGG	CTGTTTGTA	CTGCCTGCTG	TGGAGTTCC	AGACCTCCGC	TGGCCATTTC	60
CCTAGAGCCT	GTGTCTCCTC	TAAGAACCTG	ATGGAGAAGG	AATGCTGTCC	ACCGTGGAGC	120
GGGGACAGGA	GTCCCTGTGG	CCAGCTTCA	GGCAGAGGTT	CCTGTCAGAA	TATCCTTCTG	180
TCCAATGCAC	CACTTGGGCC	TCAATTCCC	TTCACAGGGG	TGGATGACCG	GGAGTCGTGG	240
CCTTCCGTCT	TTTATAATAG	GACCTGCCAG	TGCTCTGGCA	ACTTCATGGG	ATTCAACTGT	300
GGAAAATGCA	AGTTTGGCTT	TTGGGGACCA	AACTGCACAG	AGAGACGACT	CTTGGTGAGA	360
AGAAACATCT	TCGATTTGAG	TGCCCCAGAG	AAGGACAAAT	TTTTGCCTA	CCTCACTTTA	420
GCAAAGCATA	CCATCAGCTC	AGACTATGTC	ATCCCCATAG	GGACCTATGG	CCAAATGAAA	480
AATGGATCAA	CACCATGTT	TAACGACATC	AATATTATG	ACCTCTTGT	CTGGATGCAT	540
TATTATGTGT	CAATGGATGC	ACTGCTTGGG	GGATATGAAA	TCTGGAGAGA	CATTGATTTT	600
GCCCATGAAG	CACCAGCTT	TCTGCCTTGG	CATAGACTCT	TCTTGGTGC	GTGGGAACAA	660
GAAATCCAGA	AGCTGACAGG	AGATGAAAAC	TTCACTATTC	CATATTGGGA	CTGGCGGGAT	720
GCAGAAAAGT	GTGACATTG	CACAGATGAG	TACATGGAG	GTCAGCACCC	CACAAATCCT	780
AACTTACTCA	GCCCAGCATE	ATTCTTCTCC	TCTTGGCAGA	TTGTCTGTAG	CCGATTGGAG	840
GAGTACAACA	GCCATCAGTC	TTTATGCAAT	GGAACGCCCG	AGGGACCTTT	ACGGCGTAAT	900
CCTGGAAACC	ATGACAAATC	CAGAACCCCA	AGGCTCCCCT	CTTCAGCTGA	TGTAGAATT	960
TGCCTGAGTT	TGACCAATA	TGAATCTGGT	TCCATGGATA	AAGCTGCCAA	TTTCAGCTTT	1020
AGAAAATACAC	TGGAAGGATT	TGCTAGTCCA	CTTACTGGGA	TAGCGGATGC	CTCTCAAAGC	1080
AGCATGCACA	ATGCCTTGCA	CATCTATATG	AATGGAACAA	TGTCCCAGGT	ACAGGGATCT	1140
GCCAACGATC	CTATCTTCC	TCTTCACCAT	GCATTGTTG	ACAGTATT	TGAGCAGTGG	1200
CTCCGAAGGC	ACCGTCCTCT	TCAAGAAGTT	TATCCAGAAG	CCAATGCACC	CATTGGACAT	1260
AACCGGGAAAT	CCTACATGGT	TCCTTTATA	CCACTGTACA	GAAATGGTGA	TTTCTTTATT	1320
TCATCCAAG	ATCTGGGCTA	TGACTATAGC	TATCTACAAG	ATTCAAGACCC	AGACTCTTT	1380
CAAGACTACA	TTAAGTCCTA	TTTGGAACAA	GCGAGTCGGA	TCTGGTCATG	GCTCCTTGGG	1440

CGGGCGATGG TAGGGGCCGT CCTCACTGCC CTGCTGGCAG GGCTTGTGAG CTTGCTGTGT	1500
CGTCACAAGA GAAAGCAGCT TCCTGAAGAA AAGCAGCCAC TCCTCATGGA GAAAGAGGAT	1560
TACCACAGCT TGTATCAGAG CCATTAA	1587

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1587 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ATGCTCCTGG CTGTTTGTA CTGCCTGCTG TGGAGTTCC AGACCTCCGC TGGCCATTTC	60
CCTAGAGCCT GTGTCTCCTC TAAGAACCTG ATGGAGAAGG AATGCTGTCC ACCGTGGAGC	120
GGGGACAGGA GTCCCTGTGG CCAGCTTCA GGCAGAGGTT CCTGTCAGAA TATCCTCTG	180
TCCAATGCAC CACTTGGCC TCAATTCCC TTCACAGGGG TGGATGACCG GGAGTCGTGG	240
CCTTCGTCT TTTATAATAG GACCTGCCAG TGCTCTGGCA ACTTCATGGG ATTCAACTGT	300
GGAAACTGCA AGTTTGGCTT TTGGGGACCA AACTGCACAG AGAGACGACT CTTGGTGAGA	360
AGAAACATCT TCGATTTGAG TGCCCCAGAG AAGGACAAAT TTTTGCCCTA CCTCACTTTA	420
GCAAAGCATA CCATCAGCTC AGACTATGTC ATCCCCATAG GGACCTATGG CCAAATGAAA	480
AATGGATCAA CACCATGTT TAACGACATC AATATTTATG ACCTCTTGT CTGGATGCAT	540
TATTATGTGT CAATGGATGC ACTGCTTGGG GGATATGAAA TCTGGAGAGA CATTGATTTT	600
GCCCATGAAG CACCAGCTT TCTGCCTTGG CATAGACTCT TCTTGGTGGC GTGGGAACAA	660
GAAATCCAGA AGCTGACAGG AGATGAAAAC TTCACTATTC CATATTGGGA CTGGCGGGAT	720
GCAGAAAAGT GTGACATTTG CACAGATGAG TACATGGGAG GTCAGCACCC CACAAATCCT	780
AACTTACTCA GCCCAGCATC ATTCTCTCC TCTTGGCAGA TTGTCTGTAG CCGATTGGAG	840
GAGTACAACA GCCATCAGTC TTTATGCAAT GGAACGCCCG AGGGACCTT ACGGCGTAAT	900
CCTGGAAACC ATGACAAATC CAGAACCCCA AGGCTCCCT CTTCAGCTGA TGTAGAATTT	960
TGCCTGAGTT TGACCCAATA TGAATCTGGT TCCATGGATA AAGCTGCCAA TTTCAGCTTT	1020
AGAAATACAC TGGAAGGATT TGCTAGTCCA CTTACTGGGA TAGCGGATGC CTCTCAAAGC	1080
AGCATGCACA ATGCCTTGCA CATCTATATG AATGGAACAA TGTCCCAGGT ACAGGGATCT	1140
GCCAACGATC CTATCTTCCCT TCTTCACCAT GCATTGTTG ACAGTATTT TGAGCAGTGG	1200
CTCCGAAGGC ACCGTCCTCT TCAAGAAGTT TATCCAGAAG CCAATGCACC CATTGGACAT	1260
AACCAGGAAT CCTACATGGT TCCTTTATA CCACTGTACA GAAATGGTGA TTTCTTTATT	1320

TCATCCAAAG ATCTGGGCTA TGACTATAGC TATCTACAAG ATTCAAGACCC AGACTCTTTT	1380
CAAGACTACA TTAAGTCCTA TTTGGAACAA GCGAGTCGGA TCTGGTCATG GCTCCTTGGG	1440
GCGGCGATGG TAGGGGCCGT CCTCACTGCC CTGCTGGCAG GGCTTGTGAG CTTGCTGTGT	1500
CGTCACAAGA GAAAGCAGCT TCCTGAAGAA AAGCAGCCAC TCCTCATGGA GAAAGAGGAT	1560
TACCACAGCT TGTATCAGAG CCATTAA	1587

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TAAATGGCTC TGATACAAGC T	21
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(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GCAAGTTGG CTTTTGGGG	20
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(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ATGCTCCTGG CTGTTTGTA CTG	23
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(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 157 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CTGAATCTTG TAGATAGCTA TAGTCATAGC CCAGATCTTT GGATGAAATA AAGAAATCAC	60
CATTTCTGTA CAGTGGTATA AAAGGAACCA TGTAGGATTG CCGGTTATGT CTAATGGGTG	120
CATTGGCTTC TGGATAAACT TCTTGAAGAG GACGGTG	157

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 157 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

CTGAATCTTG TAGATAGCTA TAGTCATAGC CCAGATCTTT GGATGAAATA AAGAAATCAC	60
CATTTCTGTA CAGTGGTATA AAAGGAACCA TGTAGGATTG CCGGTTATGT CCAATGGGTG	120
CATTGGCTTC TGGATAAACT TCTTGAAGAG GACGGTG	157

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GGTTGGCCAA TCTACTCCCA GG	22
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(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GCTCACTCAG TGTGGCAAAG	20
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(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 536 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GGTTGGCCAA TCTACTCCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC	60
AGGGCAGAGC CATCTATTGC TTACATTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT	120
CAAACAGACA CCATGGTGCA CCTGACTCCT GAGGAGAAGT CTGCCGTTAC TGCCCTGTGG	180
GGCAAGGTGA ACGTGGATGA AGTTGGTGGT GAGGCCCTGG GCAGGTTGGT ATCAAGGTTA	240
CAAGACAGGT TTAAGGAGAC CAATAGAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG	300
TTTCTGATA GGCACTGACT CTCTCTGCCT ATTGGTCTAT TTTCCCACCC TTAGGCTGCT	360
GGTGGTCTAC CCTTGGACCC AGAGGTTCTT TGAGTCCTT GGGGATCTGT CCACTCCTGA	420
TGCTGTTATG GGCAACCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCCTTAG	480
TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTT GCCACACTGA GTGAGC	536

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 534 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GGTTGGCCAA TCTACTCCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC	60
AGGGCAGAGC CATCTATTGC TTACATTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT	120
CAAACAGACA CCATGGTGCA TCTGACTCCT GAGGAGGTCT GCCGTTACTG CCCTGTGGGG	180
CAAGGTGAAC GTGGATGAAG TTGGTGGTGA GGCCCTGGC AGGTTGGTAT CAAGGTTACA	240
AGACAGGTTT AAGGAGACCA ATAGAAACTG GGCATGTGGA GACAGAGAAG ACTCTTGGGT	300
TTCTGATAGG CACTGACTCT CTCTGCCTAT TGGTCTATTT TCCCACCCCT AGGCTGCTGG	360
TGGTCTACCC TTGGACCCAG AGGTTCTTG AGTCCTTGG GGATCTGTCC ACTCCTGATG	420
CTGTTATGGG CAACCTAAG GTGAAGGCTC ATGGCAAGAA AGTGCTCGGT GCCTTTAGTG	480
ATGGCCTGGC TCACCTGGAC AACCTCAAGG GCACCTTGC CACACTGAGT GAGC	534

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 536 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GGTTGGCAA TCTACTCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC	60
AGGGCAGAGC CATCTATTGC TTACATTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT	120
CAAACAGACA CCATGGTGCA CCTGACTCCT GAGGAGAACT CTGCCGTTAC TGCCCTGTGG	180
GGCAAGGTGA ACGTGGATGA AGTTGGTGGT GAGGCCCTGG GCAGGTTGGT ATCAAGGTTA	240
CAAGACAGGT TTAAGGAGAC CAATAGAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG	300
GTTTCTGATA GGCAC TGACT CTCTCTGCCT ATTGGTCTAT TTTCCCACCC TTAGGCTGCT	360
GGTGGTCTAC CCTTGGACCT AGAGGTTCTT TGAGTCCTT GGGGATCTGT CCACTCCTGA	420
TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCTTAG	480
TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC	536

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GGTTGGCAA TCTACTCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC	60
AGGGCAGAGC CATCTATTGC TTACATTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT	120
CAAACAGACA CCATGGTGCA CCTGACTCCT GAGGAGAACT CTGCCGTTAC TGCCCTGTGG	180
GGCAAGGTGA ACGTGGATGA AGTTGGAGGT GAGGCCCTGG GCAGGTTGGT ATCAAGGTTA	240
CAAGACAGGT TTAAGGAGAC CAATAGAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG	300
GTTTCTGATA GGCAC TGACT CTCTCTGCCT ATTGGTCTAT TTTCCCACCC TTAGGCTGCT	360
GGTGGTCTAC CCTTGGACCC AGAGGTTCTT TGAGTCCTT GGGGATCTGT CCACTCCTGA	420
TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCTTAG	480
TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC	536

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GAAUACUCAA GCUUGCAUGC CUGCAGGUUCG ACUCUAGAGG AUCCCCGGGU ACCGAGCUCG 60  
AAUU 64

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GGCTGACAAG AAGGAAACTC 20

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CCAGGCGGCG GCTAGGAGAG ATGGG 25

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 351 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GGCTGACAAG AAGGAAACTC GCTGAGACAG CAGGGACTTT CCACAAGGGG ATGTTACGGG 60  
GAGGTACTGG GGAGGAGCCG GTCGGGAACG CCCACTCTCT TGATGTATAA ATATCACTGC 120  
ATTCGCTCT GTATTCAGTC GCTCTGCGGA GAGGCTGGCA GATTGAGCCC TGGGAGGTTTC 180  
TCTCCAGCAC TAGCAGGTAG AGCCTGGGTG TTCCCTGCTA GACTCTCACC AGCACTTGGC 240  
CGGTGCTGGG CAGAGTGGCT CCACGCTTGC TTGCTTAAAG ACCTCTTCAA TAAAGCTGCC 300  
ATTTTAGAAG TAGGCCAGTG TGTGTTCCA TCTCTCCTAG CCGCCGCCCTG G 351

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 340 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GGCTGACAAG AAGGAAACTC GCTGAGATAG CAGGGACTTT CCACAAGGGG ATGTTATGGG	60
GAGGAGCCGG TCGGGAACAC CCACCTTCTT GATGTATAAA TATCACTGCA TTTCGCTCTG	120
TATTCAGTCG CTCTGCGGAG AGGCTGGCAG ATTGAGCCCT GGGAGGTTCT CTCCAGCACT	180
AGCAGGTAGA GCCTGGGTGT TCCCTGCTAG ACTCTCACCA GCACCTAGCC AGTGCTGGC	240
AGAGTGGCTC CACGCTTGCT TGCTTAAAGA CCTCTTCAAT AAAGCTGCCA TTTAGAAGT	300
AAGCCAGTGT GTGTTCCCAT CTCTCCTAGC CGCCGCCTGG	340

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 340 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GGCTGACAAG AAGGAAACTC GCTGAGATAG CAGGGACTTT CCACAAGGGG ATGTTATGGG	60
GAGGAGCCGG TCGGGAACAC CCACCTTCTT GGTGTATAAA TATCACTGCA TTTCGCTCTG	120
TATTCAGTCG CTCTGCGGAG AGGCTGGCAG ATTGAGCCCT GGGAGGTTCT CTCCAGCACT	180
AGCAGGTAGA GCCTGGGTGT TCCCTGCTAG ACTCTCACCA GCACCTGGCC AGTGCTGGC	240
AGAGTGGCTC CACGCTTGCT TGCTTAAAGA CCTCTTCAAT AAAGCTGCCA TTTAGAAGT	300
AAGCCAGTGT GTGTTCCCAT CTCTCCTAGC CGCCGCCTGG	340

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 351 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GGCTGACAAG AAGGAAACTC GCTGAGACAG CAGGGACTTT CCACAAGGGG ATGTTACGGG	60
GAGGTACTGG GGAGGAGCCG GTCGGGAACG CCCACTCTCT TGATGTATAA ATATCACTGC	120
ATTCGCTCT GTATTCAAGTC GCTCTGCGGA GAGGCTGGCA GATTGAGCCC TGGGAGGTTC	180
TCTCCAGCAC TAGCAGGTAG AGCCTGGGTG TTCCCTGCTA GACTCTCACC AGCACTTGGC	240
CGGTGCTGGG CAGAGTGGCT CCACGCTTGC TTGCTTAAAG ACCTCTCAA TAAAGCTGCC	300
ATTTAGAAG TAGGCTAGTG TGTGTTCCCA TCTCTCCTAG CCGCCGCCTG G	351

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 351 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GGCTGACAAG AAGGAAACTC GCTGAAACAG CAGGGACTTT CCACAAGGGG ATGTTACGGG	60
GAGGTACTGG GAAGGAGCCG GTCGGGAACG CCCACTTTCT TGATGTATAA ATATCACTGC	120
ATTCGCTCT GTATTCAAGTC GCTCTGCGGA GAGGCTGGCA GATTGAGCCC TGGGAGGTTC	180
TCTCCAGCAC TAGCAGGTAG AGCCTGGGTG TTCCCTGCTA GACTCTCACC AGCACTTGGC	240
CGGTGCTGGG CAGAGTGAAT CCACGCTTGC TTGCTTAAAG CCCTCTCAA TAAAGCTGCC	300
ATTTAGAAG TAAGCTAGTG TGTGTTCCCA TCTCTCCTAG CCGCCGCCTG G	351

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 351 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GGCTGACAAG AAGGAAACTC GCTGAGACAG CAGGGACTTT CCACAAGGGG ATGTTACGGA	60
GAGGTACTGG GGAGGAGCCG GTCGGGAACG CCCACTCTCT TGATGTATAA ATATCACTGC	120
ATTCGCTCT GTATTCAAGTC GCTCTGCGGA GAGGCTGGCA GATTGAGCCC TAGGAGGTTC	180
TCTCCAGCAC TAGCAGGTAG AGCCTGAGTG TTCCCTGCTA AACTCTCACC AGCACTTGGC	240
CGGTGCTGGG CAGAGCGGCT CCACGCTTGC TTGCTTAAAG ACCTCTCAA TAAAGCTGCC	300
ATTTAGAAG TAGGCTAGTG TGTGTTCCCA TCTCTCCTAG CCGCCGCCTG G	351

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 536 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GGTTGGCAA TCTACTCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC	60
AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT	120
CAAACAGACA CCATGGTGCA TCTGACTCCT GAGGAGAAAGT CTGCCGTTAC TGCCCTGTGG	180
GGCAAGGTGA ACGTGGATGA AGTTGGTGGT AAGGCCCTGG GCAGGTTGGT ATCAAGGTTA	240
CAAGACAGGT TTAAGGAGAC CAATAGAAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG	300
GTTTCTGATA GGCACTGACT CTCTCTGCCT ATTGGTCTAT TTTCCCACCC TTAGGCTGCT	360
GGTGGTCTAC CCTTGGACCC AGAGGTTCTT TGAGTCCTT GGGGATCTGT CCACTCCTGA	420
TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCCTTAG	480
TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC	536

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 536 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GGTTGGCAA TCTACTCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC	60
AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT	120
CAAACAGACA CCATGGTGCA CCTGACTCCT GAGGAGAAAGT CTGCCGTTAC TGCCCTGTGG	180
GGCAAGGTGA ACGTGGATGA AGTTGGTGGT GAGGCCCTGG GCAGGTTGGT ATCAAGGTTA	240
CAAGACAGGT TTAAGGAGAC CAATAGAAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG	300
GTTTCTGATA GGCACTGACT CTCTCTGCCT ATTAGTCTAT TTTCCCACCC TTAGGCTGCT	360
GGTGGTCTAC CCTTGGACCC AGAGGTTCTT TGAGTCCTT GGGGATCTGT CCACTCCTGA	420
TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCCTTAG	480
TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC	536

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 157 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCAGGAA	60
TCCTACATGG TTCCTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTAT TTCATCCAAA	120
GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAAG	157

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 833 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu			
1	5	10	15
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys			
20	25	30	
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe			
35	40	45	
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile			
50	55	60	
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly			
65	70	75	80
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln			
85	90	95	
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu			
100	105	110	
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys			
115	120	125	
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys			
130	135	140	
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu			
145	150	155	160
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg			
165	170	175	

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu  
 355 360 365  
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn  
 405 410 415  
 Leu Trp Gly Arg Leu Glu Gly Glu Arg Leu Leu Trp Leu Tyr Arg  
 420 425 430  
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val  
 450 455 460  
 Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495

Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys  
 500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525

Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser  
 530 535 540

Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg  
 545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590

Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
 595 600 605

Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685

Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700

Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
 705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Tyr Val Pro Asp Leu Glu Ala  
 725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750

Pro Val Arg Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780

His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
 785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
820 825 830

Glu

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 548 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335

Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu  
 340 345 350

Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu  
 355 360 365

Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400

Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn  
 405 410 415

Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg  
 420 425 430

Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr  
 435 440 445

Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val  
 450 455 460

Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495

Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys  
 500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525

Ile Val Glu Lys Ile Leu Gln Ala Cys Lys Leu Gly Thr Gly Arg Arg  
 530 535 540

Phe Thr Thr Ser  
 545

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 695 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu  
 355 360 365  
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn  
 405 410 415  
 Leu Trp Gly Arg Leu Glu Gly Glu Arg Leu Leu Trp Leu Tyr Arg  
 420 425 430  
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val  
 450 455 460  
 Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys  
 500 505 510  
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser  
 530 535 540  
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
 595 600 605

Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640  
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ser His Pro Leu  
 675 680 685  
 Arg Gly Gly Pro Gly Leu His  
 690 695

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
 1 5 10 15  
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
 20 25 30  
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
 35 40 45  
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
 50 55 60  
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
 65 70 75 80  
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
 85 90 95  
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
 100 105 110  
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
 115 120 125  
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
 130 135 140  
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
 145 150 155 160  
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ser Trp Arg Gly Cys Ile Pro Trp Pro Cys Pro  
 290 295 300  
 Trp Arg Trp Arg Trp Gly  
 305 310

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 322 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Asn Ser Gly  
 1 5 10 15  
 Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly  
 20 25 30  
 His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu Thr Thr  
 35 40 45  
 Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu  
 50 55 60  
 Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val Phe Asp  
 65 70 75 80  
 Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr Lys Ala  
 85 90 95  
 Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala Leu Ile  
 100 105 110  
 Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu Val Pro Gly  
 115 120 125

Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys Ala Glu Lys  
 130 135 140  
 Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu Tyr Gln  
 145 150 155 160  
 Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr Leu Ile  
 165 170 175  
 Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp Gln Trp  
 180 185 190  
 Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu Pro Gly  
 195 200 205  
 Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp  
 210 215 220  
 Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala  
 225 230 235 240  
 Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu Ser Trp  
 245 250 255  
 Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp Phe Ala  
 260 265 270  
 Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe Leu Glu Arg  
 275 280 285  
 Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro  
 290 295 300  
 Lys Ser Trp Arg Gly Cys Ile Pro Trp Pro Cys Pro Trp Arg Trp Arg  
 305 310 315 320  
 Trp Gly

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 528 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly  
 1 5 10 15  
 His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu Thr Thr  
 20 25 30  
 Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu  
 35 40 45  
 Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val Phe Asp  
 50 55 60

Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr Lys Ala  
 65 70 75 80  
 Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala Leu Ile  
 85 90 95  
 Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu Val Pro Gly  
 100 105 110  
 Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys Ala Glu Lys  
 115 120 125  
 Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu Tyr Gln  
 130 135 140  
 Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr Leu Ile  
 145 150 155 160  
 Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp Gln Trp  
 165 170 175  
 Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu Pro Gly  
 180 185 190  
 Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp  
 195 200 205  
 Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala  
 210 215 220  
 Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu Ser Trp  
 225 230 235 240  
 Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp Phe Ala  
 245 250 255  
 Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe Leu Glu Arg  
 260 265 270  
 Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro  
 275 280 285  
 Lys Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala  
 290 295 300  
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly  
 305 310 315 320  
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr  
 325 330 335  
 Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro  
 340 345 350  
 Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly  
 355 360 365  
 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu  
 370 375 380  
 Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg  
 385 390 395 400

Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val  
 405 410 415  
 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg  
 420 425 430  
 Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro  
 435 440 445  
 Val Arg Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu  
 450 455 460  
 Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His  
 465 470 475 480  
 Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala  
 485 490 495  
 Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro  
 500 505 510  
 Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu  
 515 520 525

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 315 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Asn Ser Gly  
 1 5 10 15  
 Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly  
 20 25 30  
 His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu Thr Thr  
 35 40 45  
 Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu  
 50 55 60  
 Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val Phe Asp  
 65 70 75 80  
 Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr Lys Ala  
 85 90 95  
 Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala Leu Ile  
 100 105 110  
 Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu Val Pro Gly  
 115 120 125

Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys Ala Glu Lys  
 130 135 140

Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu Tyr Gln  
 145 150 155 160

Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr Leu Ile  
 165 170 175

Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp Gln Trp  
 180 185 190

Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu Pro Gly  
 195 200 205

Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp  
 210 215 220

Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala  
 225 230 235 240

Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu Ser Trp  
 245 250 255

Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp Phe Ala  
 260 265 270

Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe Leu Glu Arg  
 275 280 285

Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro  
 290 295 300

Lys Ala Ala Leu Glu His His His His His His  
 305 310 315

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATGGAGGAGC CGCAGTCAGA TCCTAGCGTC GAGCCCCCTC TGAGTCAGGA AACATTTCA	60
GACCTATGGA AACTACTTCC TGAAAACAAAC GTTCTGTCCC CCTTGCCGTC CCAAGCAATG	120
GATGATTGTA TGCTGTCCCC GGACGATATT GAACAAATGGT TCACTGAAGA CCCAGGTCCA	180
GATGAAGCTC CCAGAAATGCC AGAGGCTGCT CCCCCCGTGG CCCCTGCACC AGCAGCTCCT	240
ACACCGGGCGG CCCCTGCACC AGCCCCCTCC TGGCCCCTGT CATCTTCTGT CCCTTCCCAG	300
AAAACCTACC AGGGCAGCTA CGGTTTCCGT CTGGGCTTCT TGCATTCTGG GACAGCCAAG	360
TCTGTGACTT GCACGTACTC CCCTGCCCTC AACAAAGATGT TTTGCCAACT GGCCAAGACC	420

TGCCCTGTGC AGCTGTGGGT TGATTCCACA CCCCCGCCCG GCACCCGCGT CCGCGCCATG	480
GCCATCTACA AGCAGTCACA GCACATGACG GAGGTTGTGA GGCGCTGCC CCACCATGAG	540
CGCTGCTCAG ATAGCGATGG TCTGGCCCT CCTCAGCATC TTATCCGAGT GGAAGGAAAT	600
TTGCGTGTGG AGTATTTGGA TGACAGAAAC ACTTTTCGAC ATAGTGTGGT GGTGCCCTAT	660
GAGCCGCCTG AGGTTGGCTC TGACTGTACC ACCATCCACT ACAACTACAT GTGTAACAGT	720
TCCTGCATGG GCGGCATGAA CCGGAGGCC ATCCTCACCA TCATCACACT GGAAGACTCC	780
AGTGGTAATC TACTGGGACG GAACAGCTT GAGGTGCGTG TTTGTGCCG 720	840
GACCGGGCGCA CAGAGGAAGA GAATCTCCGC AAGAAAGGGG AGCCTCACCA CGAGCTGCC	900
CCAGGGAGCA CTAAGCGAGC ACTGCCAAC AACACCAGCT CCTCTCCCCA GCCAAAGAAG	960
AAACCACTGG ATGGAGAATA TTTCACCCCT CAGATCCGTG GGCGTGAGCG CTTCGAGATG	1020
TTCCGAGAGC TGAATGAGGC CTTGGAACTC AAGGATGCC AGGCTGGAA GGAGCCAGGG	1080
GGGAGCAGGG CTCACTCCAG CCACCTGAAG TCCAAAAGG GTCAGTCTAC CTCCGCCAT	1140
AAAAAAACTCA TGTTCAAGAC AGAAGGGCCT GACTCAGACT GA	1182

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1182 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATGGAGGAGC CGCAGTCAGA TCCTAGCGTC GAGCCCCCTC TGAGTCAGGA AACATTTCA	60
GACCTATGGA AACTACTTCC TGAAAACAAC GTTCTGTCCC CCTTGCGCGTC CCAAGCAATG	120
GATGATTGAGA TGCTGTCCCC GGACGATATT GAACAATGGT TCACTGAAGA CCCAGGTCCA	180
GATGAAGCTC CCAGAATGCC AGAGGCTGCT CCCCCCGTGG CCCCTGCACC AGCAGCTCCT	240
ACACCGGGCGG CCCCTGCACC AGCCCCCTCC TGGCCCTGT CATCTTCTGT CCCTTCCCAG	300
AAAACCTACC AGGGCAGCTA CGGTTTCCGT CTGGGCTTCT TGCATTCTGG GACAGCCAAG	360
TCTGTGACTT GCACGTACTC CCCTGCCCTC AACAAAGATGT TTTGCCAACT GGCCAAGACC	420
TGCCCTGCGC AGCTGTGGGT TGATTCCACA CCCCCGCCCG GCACCCGCGT CCGCGCCATG	480
GCCATCTACA AGCAGTCACA GCACATGACG GAGGTTGTGA GGCGCTGCC CCACCATGAG	540
CGCTGCTCAG ATAGCGATGG TCTGGCCCT CCTCAGCATC TTATCCGAGT GGAAGGAAAT	600
TTGCGTGTGG AGTATTTGGA TGACAGAAAC ACTTTTCGAC ATAGTGTGGT GGTGCCCTAT	660
GAGCCGCCTG AGGTTGGCTC TGACTGTACC ACCATCCACT ACAACTACAT GTGTAACAGT	720

TCCTGCATGG CGGGCATGAA CCGGAGGCCC ATCCTCACCA TCATCACACT GGAAGACTCC	780
AGTGGTAATC TACTGGGACG GAACAGCTT GAGGTGCGTG TTTGTGCCTG TCCTGGGAGA	840
GACCGGCGCA CAGAGGAAGA GAATCTCCGC AAGAAAGGGG AGCCTCACCA CGAGCTGCC	900
CCAGGGAGCA CTAAGCGAGC ACTGCCAAC AACACCAGCT CCTCTCCCCA GCCAAAGAAG	960
AAACCACTGG ATGGAGAATA TTTCACCCCTT CAGATCCGTG GGCGTGAGCG CTTCGAGATG	1020
TTCCGAGAGC TGAATGAGGC CTTGGAACTC AAGGATGCC AGGCTGGAA GGAGCCAGGG	1080
GGGAGCAGGG CTCACTCCAG CCACCTGAAG TCCAAAAGG GTCAGTCTAC CTCCCGCCAT	1140
AAAAAACTCA TGTTCAAGAC AGAAGGGCCT GACTCAGACT GA	1182

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1182 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATGGAGGAGC CGCAGTCAGA TCCTAGCGTC GAGCCCCCTC TGAGTCAGGA AACATTTCA	60
GACCTATGGA AACTACTTCC TGAAAACAAC GTTCTGTCCC CCTTGCCGTC CCAAGCAATG	120
GATGATTTGA TGCTGTCCCC GGACGATATT GAACAATGGT TCACTGAAGA CCCAGGTCCA	180
GATGAAGCTC CCAGAAATGCC AGAGGCTGCT CCCCCCGTGG CCCCTGCACC AGCAGCTCCT	240
ACACCGGGCGG CCCCTGCACC AGCCCCCTCC TGGCCCTGT CATCTTCTGT CCCTTCCCAG	300
AAAACCTACC AGGGCAGCTA CGGTTCCGT CTGGGCTTCT TGCATTCTGG GACAGCCAAG	360
TCTGTGACTT GCACGTACTC CCCTGCCCTC AACAAAGATGT TTTGCCAACT GGCCAAGACC	420
TGCCCTGTGC AGCTGTGGGT TGATTCCACA CCCCCGCCCC GCACCCCGGT CCGCGCCATG	480
GCCATCTACA AGCAGTCACA GCACATGACG GAGGTTGTGA GGCGCTGCC CCACCATGAG	540
CGCTGCTCAG ATAGCGATGG TCTGGCCCT CCTCAGCATC TTATCCGAGT GGAAGGAAAT	600
TTGCGTGTGG AGTATTTGGA TGACAGAAAC ACTTTTCGAC ATAGTGTGGT GGTGCCCTAT	660
GAGCCGCCTG AGGTTGGCTC TGACTGTACC ACCATCCACT ACAACTACAT GTGTAACAGT	720
TCCTGCATGG CGGGCATGAA CCGGAGACCC ATCCTCACCA TCATCACACT GGAAGACTCC	780
AGTGGTAATC TACTGGGACG GAACAGCTT GAGGTGCGTG TTTGTGCCTG TCCTGGGAGA	840
GACCGGCGCA CAGAGGAAGA GAATCTCCGC AAGAAAGGGG AGCCTCACCA CGAGCTGCC	900
CCAGGGAGCA CTAAGCGAGC ACTGCCAAC AACACCAGCT CCTCTCCCCA GCCAAAGAAG	960
AAACCACTGG ATGGAGAATA TTTCACCCCTT CAGATCCGTG GGCGTGAGCG CTTCGAGATG	1020

TTCCGAGAGC TGAATGAGGC CTTGGAACTC AAGGATGCCC AGGCTGGAA GGAGCCAGGG	1080
GGGAGCAGGG CTCACTCCAG CCACCTGAAG TCCAAAAGG GTCAGTCTAC CTCCCGCCAT	1140
AAAAAACTCA TGTTCAAGAC AGAAGGGCCT GACTCAGACT GA	1182

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TCTGGGCTTC TTGCATTCTG	20
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(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GTTGGGCAGT GCTCGCTTAG	20
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(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 601 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT	60
CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC	120
ACCCCCGCCCG GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC	180
GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC	240
TCCTCAGCAT CTTATCCGAG TGGAAAGGAAA TTTGCGTGTG GAGTATTGG ATGACAGAAA	300
CACTTTTCGA CATACTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC	360
CACCATCCAC TACAACCTACA TGTGTAACAG TTCCCTGCATG GGCGGCATGA ACCGGAGGCC	420
CATCCTCACCA ATCATCACAC TGGAAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT	480

TGAGGTGCGT GTTTGTGCCT GTCCTGGAG AGACCGGCGC ACAGAGGAAG AGAATCTCCG	540
CAAGAAAGGG GAGCCTCACC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCAA	600
C	601

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GTTGGGCAGT GCTCGCTTAG TGCTCCCTGG GGGCAGCTCG TGGTGAGGCT CCCCTTTCTT	60
CGGGAGATTTC TCTTCCTCTG TGCGCCGGTC TCTCCCAGGA CAGGCACAAA CACGCACCTC	120
AAAGCTGTTTC CGTCCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT	180
GGGCCTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT	240
GGTACAGTCA GAGCCAACCT CAGGCGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT	300
GTTTCTGTCA TCCAAATACT CCACACGCAA ATTTCTTCC ACTCGGATAA GATGCTGAGG	360
AGGGGCCAGA CCATCGCTAT CTGAGGCAGCG CTCATGGTGG GGGCAGCGCC TCACAAACCTC	420
CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCGG ACGCGGGTGC CGGGCGGGGG	480
TGTGGAATCA ACCCACAGCT GCACAGGGCA GGTCTTGGCC AGTTGGCAAA ACATCTTGT	540
GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAAGCCCAG	600
A	601

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT	60
CAACAAGATG TTTTGCCAAAC TGGCCAAGAC CTGCCCTGCG CAGCTGTGGG TTGATTCCAC	120
ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC	180
GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC	240
TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGGCTGTG GAGTATTGG ATGACAGAAA	300

CACTTTCTGA CATACTGTGG TGGTGCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC	360
CACCATCCAC TACAATACA TGTGTAACAG TTCCTGCATG GGCGGCATGA ACCGGAGGCC	420
CATCCTCACCC ATCATCACAC TGGAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT	480
TGAGGTGCGT GTTGTGCCT GTCCTGGAG AGACCGGCGC ACAGAGGAAG AGAATCTCCG	540
CAAGAAAGGG GAGCCTCACCC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCAA	600
C	601

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 601 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GTTGGGCAGT GCTCGCTTAG TGCTCCCTGG GGGCAGCTCG TGGTGAGGCT CCCCTTTCTT	60
GCGGAGATTC TCTTCCTCTG TCGGCCGGTC TCTCCCAGGA CAGGCACAAA CACGCACCTC	120
AAAGCTGTTC CGTCCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT	180
GGGCCTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT	240
GGTACAGTCA GAGCCAACCT CAGGCGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT	300
GTTTCTGTCA TCCAAATACT CCACACGCAA ATTTCTTCC ACTCGGATAA GATGCTGAGG	360
AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGGCAGCGCC TCACAACCTC	420
CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCGG ACGCGGGTGC CGGGCGGGGG	480
TGTGGAATCA ACCCACAGCT GCGCAGGGCA GGTCTTGGCC AGTTGGCAAA ACATCTTGT	540
GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAAGCCCAG	600
A	601

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 601 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT	60
CAACAAGATG TTTTGCCAAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC	120

ACCCCCGCC	GGCACCCGCG	TCCGCGCCAT	GGCCATCTAC	AAGCAGTCAC	AGCACATGAC	180
GGAGGTTGTG	AGGCGCTGCC	CCCACCATGA	GCGCTGCTCA	GATAGCGATG	GTCTGGCCCC	240
TCCTCAGCAT	CTTATCCGAG	TGGAAGGAAA	TTTGCCTGTG	GAGTATTG	ATGACAGAAA	300
CACTTTCGA	CATAGTGTGG	TGGTGCCTA	TGAGCCGCCT	GAGGTTGGCT	CTGACTGTAC	360
CACCATCCAC	TACAAC TACA	TGTGTAACAG	TTCCCTGCATG	GGCGGCATGA	ACCGGAGACC	420
CATCCTCACC	ATCATCACAC	TGGAAGACTC	CAGTGGTAAT	CTACTGGGAC	GGAACAGCTT	480
TGAGGTGCGT	GTGGTGCCT	GTCCTGGAG	AGACCGGCGC	ACAGAGGAAG	AGAATCTCCG	540
CAAGAAAGGG	GAGCCTCACC	ACGAGCTGCC	CCCAGGGAGC	ACTAAGCGAG	CACTGCCAA	600
C						601

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 601 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GTTGGGCAGT	GCTCGCTTAG	TGCTCCCTGG	GGGCAGCTCG	TGGTGAGGCT	CCCCTTTCTT	60
CGGGAGATT	CCTTCCTCTG	TGCGCCGGTC	TCTCCCAGGA	CAGGCACAAA	CACGCACCTC	120
AAAGCTGTT	CGTCCCAGTA	GATTACCACT	GGAGTCTTCC	AGTGTGATGA	TGGTGGAGGAT	180
GGGTCTCCGG	TTCATGCCGC	CCATGCAGGA	ACTGTTACAC	ATGTAGTTGT	AGTGGATGGT	240
GGTACAGTCA	GAGCCAACCT	CAGGCGGCTC	ATAGGGCACC	ACCACACTAT	GTCGAAAAGT	300
GTTTCTGTCA	TCCAAATACT	CCACACGCAA	ATTTCTTCC	ACTCGGATAA	GATGCTGAGG	360
AGGGGCCAGA	CCATCGCTAT	CTGAGCAGCG	CTCATGGTGG	GGGCAGCGCC	TCACAACCTC	420
CGTCATGTGC	TGTGACTGCT	TGTAGATGGC	CATGGCGCGG	ACGCGGGTGC	CGGGCGGGGG	480
TGTGGAATCA	ACCCACAGCT	GCACAGGGCA	GGTCTTGGCC	AGTTGGCAAA	ACATCTTGT	540
GAGGGCAGGG	GAGTACGTGC	AAGTCACAGA	CTTGGCTGTC	CCAGAATGCA	AGAAGCCCAG	600
A						601

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GAGGATGGGA CTCCGGTTCA TG

22

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CATGAACCGG AGTCCCATCC TCAC

24

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GCACAAACAT GCACCTCAAA GCT

23

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CAGCTTGAG GTGCATGTT GT

22

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT	60
CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC	120
ACCCCCGCCCG GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC	180
GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC	240
TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTGG ATGACAGAAA	300
CACTTTTCGA CATACTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC	360
CACCATCCAC TACAACATACA TGTGTAACAG TTCCCTGCATG GGCGGCATGA ACCGGAGTCC	420
CATCCTCACC ATCATCACAC TGGAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT	480
TGAGGTGCGT GTTTGTGCCT GTCCTGGAG AGACCGGCAG ACAGAGGAAG AGAATCTCCG	540
CAAGAAAGGG GAGCCTCACC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCAA	600
C	601

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GTTGGGCAGT GCTCGCTTAG TGCTCCCTGG GGGCAGCTCG TGGTGAGGCT CCCCTTTCTT	60
CGGGAGATTG TCTTCCTCTG TGCGCCGGTC TCTCCCAGGA CAGGCACAAA CACGCACCTC	120
AAAGCTGTTG CGTCCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT	180
GGGACTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT	240
GGTACAGTCA GAGCCAACCT CAGGCGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT	300
GTTCCTGTCA TCCAAATACT CCACACGCAA ATTTCTTCC ACTCGGATAA GATGCTGAGG	360
AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGGCAGCGCC TCACAAACCTC	420
CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCGG ACGCGGGTGC CGGGCGGGGG	480
TGTGGAATCA ACCCACAGCT GCACAGGGCA GGTCTTGGCC AGTTGGCAAA ACATCTTGTG	540
GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAAGCCCAG	600
A	601

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 601 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT	60
CAACAAAGATG TTTTGCCAAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC	120
ACCCCCGCCCG GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC	180
GGAGGTTGTG AGGCCTGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC	240
TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTGAG ATGACAGAAA	300
CACTTTCGA CATAGTGTGG TGGTGCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC	360
CACCATCCAC TACAACCTACA TGTGTAACAG TTCCCTGCATG GGCGGCATGA ACCGGAGGCC	420
CATCCTCACCC ATCATCACAC TGGAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT	480
TGAGGTGCAT GTTGTGCCT GTCCTGGGAG AGACCGGCAG ACAGAGGAAG AGAATCTCCG	540
CAAGAAAAGGG GAGCCTCACC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCAA	600
C	601

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 601 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GTTGGGCAGT GCTCGCTTAG TGCTCCCTGG GGGCAGCTCG TGGTGAGGCT CCCCTTTCTT	60
GCGGAGATTC TCTTCCTCTG TCGGCCGGTC TCTCCCAGGA CAGGCACAAA CATGCACCTC	120
AAAGCTGTTC CGTCCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT	180
GGGCCTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT	240
GGTACAGTCA GAGCCAACCT CAGGCGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT	300
GTTTCTGTCA TCCAAATACT CCACACGCAA ATTTCCCTCC ACTCGGATAA GATGCTGAGG	360
AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGGCAGCGCC TCACAAACCTC	420
CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCGG ACGCGGGTGC CGGGCGGGGG	480

TGTGGAATCA ACCCACAGCT GCACAGGGCA GGTCTTGGCC AGTTGGAAA ACATCTTGT 540  
GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAAGCCCAG 600  
A 601

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 427 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT 60  
CAACAAGATG TTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC 120  
ACCCCCGCCCG GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC 180  
GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC 240  
TCCTCAGCAT CTTATCCGAG TGGAAAGGAAA TTTGCGTGTG GAGTATTIGG ATGACAGAAA 300  
CACTTTTCGA CATACTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC 360  
CACCATCCAC TACAACATACA TGTGTAACAG TTCCTGCATG GGCGGCATGA ACCGGAGTCC 420  
CATCCTC 427

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 196 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CATGAACCGG AGTCCCATCC TCACCATCAT CACACTGGAA GACTCCAGTG GTAATCTACT 60  
GGGACGGAAC AGCTTGAGG TGCCTGTTG TGCCCTGCCT GGGAGAGACC GGCGCACAGA 120  
GGAAGAGAAAT CTCCGCAAGA AAGGGGAGCC TCACCAAGAG CTGCCCCCAG GGAGCACTAA 180  
GCGAGCACTG CCCAAC 196

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 498 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT	60
CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC	120
ACCCCCGCCCG GGCACCCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC	180
GGAGGTTGTG AGGCGCTGCC CCCACCAGTA GCGCTGCTCA GATAGCGATG GTCTGGCCCC	240
TCCTCAGCAT CTTATCCGAG TGGAAAGGAAA TTTGCGTGTG GAGTATTGAG ATGACAGAAA	300
CACTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC	360
CACCATCCAC TACAACATACA TGTGTAACAG TTCCTGCATG GGCGGCATGA ACCGGAGGCC	420
CATCCTCACCATCACAC TGGAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT	480
TGAGGTGCAT GTTTGTGC	498

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

CAGCTTGAG GTGCATGTTT GTGCCTGTCC TGGGAGAGAC CGGCGCACAG AGGAAGAGAA	60
TCTCCGCAAG AAAGGGGAGC CTCACCACGA GCTGCCCTCA GGGAGCACTA AGCGAGCACT	120
GCCCAAC	127

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GGTTTTCTT TGAGGTTAG	20
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(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:  
GCGACACTCC ACCATAGAT 19

(2) INFORMATION FOR SEQ ID NO:117:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:  
CTGTCTTCAC GCAGAAAGC 19

(2) INFORMATION FOR SEQ ID NO:118:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:  
GCACGGTCTA CGAGACCTC 19

(2) INFORMATION FOR SEQ ID NO:119:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:  
GATCTACTAG TCATATGGAT 20

(2) INFORMATION FOR SEQ ID NO:120:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:  
TCGGTACCCG GGGATCCGAT 20

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

CTGTCTTCAC GCAGAAAGCG TCTGGCCATG GCGTTAGTAT GAGTGTCTG CAGCCTCCAG	60
GACCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC	120
CAGGACGACC GGGTCCTTTC TTGGATAAAC CCGCTCAATG CCTGGAGATT TGGGCGTGCC	180
CCCGCAAGAC TGCTAGCCGA GTAGTGTGG GTCGCGAAAG GCCTGTGGT ACTGCCTGAT	240
AGGGTGCCTG CGAGTGCCTT GGGAGGTCTC GTAGACCGTG C	281

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

CTGTCTTCAC GCAGAAAGCG TCTGGCCATG GCGTTAGTAT GAGTGTCTG CAGCCTCCAG	60
GACCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGACTGTC TTCACGCAGA	120
AAGCGTCTAG CCATGGCGTT AGTATGAGTG TCGTGCAGCC TCCAGGACCC CCCCTCCGG	180
GAGAGCCATA GTGGTCTGCG GAACCGGTGA GTACACCGGA ATTGCCAGGA CGACCGGGTC	240
CTTTCTTGGT TCAACCCGCT CAATGCCTGG AGATTTGGGC GTGCCCGCGC AAGACTGCTA	300
GCCGAGTAGT GTTGGGTCGC GAAAGGCCTT GTGGTACTGC CTGATAGGGT GCTTGCAGT	360
GCCCCGGGAG GTCTCGTACA CCGTGC	386

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

CTGTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCGTG CAGCCTCCAG	60
GTCCCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC	120
CAGGACGACC GGGTCCTTTC TTGGATCAAC CCGCTCAATG CCTGGAGATT TGGGCGTGCC	180
CCCGCGAGAC TGCTAGCCGA GTAGTGTGG GTCGCGAAAG GCCTTGTGGT ACTGCCTGAT	240
AGGGTGCTTG CGAGTCCCCC GGGAGGTCTC GTAGACCGTG C	281

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

CTGTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCGTG CAGCCTCCAG	60
GACCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC	120
CAGGACGACC GGGTCCTTTC GTGGATGTAA CCCGCTCAAT GCCTGGAGAT TTGGGCGTGC	180
CCCCGCAAGA CTGCTAGCCG AGTAGTGTG GGTGCGAAA GGCCTTGTGG TACTGCCTGA	240
TAGGGTGCTT GCGAGTCCCCC CGGGAGGTCTC CGTAGACCGTG GC	282

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

CTGTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCGTA CAGCCTCCAG	60
GCCCCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC	120
CGGGGAAGACT GGGTCCTTTC TTGGATAAAC CCACTCTATG CCCGGCCATT TGGGCGTGCC	180
CCCGCAAGAC TGCTAGCCGA GTAGCGTTGG GTTGCAGAAAG GCCTTGTGGT ACTGCCTGAT	240
AGGGTGCTTG CGAGTACCCCC GGGAGGTCTC GTAGACCGTG C	281

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 281 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

CTGTCTTCAC GCAGAAAGCG CCTAGCCATG GCGTTAGTAC GAGTGTCTG CAGCCTCCAG	60
GACCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	120
TGGGGTGACC GGGTCCTTTC TTGGAGCAAC CCGCTCAATA CCCAGAAATT TGGGCGTGCC	180
CCCGCGAGAT CACTAGCCGA GTAGTGTGG GTCGCGAAAG GCCTTGTGGT ACTGCCTGAT	240
AGGGTGCTTG CGAGTGCCCC GGGAGGTCTC GTAGACCGTG C	281

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 281 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAGGCACCC TATCAGGCAG TACCACAAGG	60
CCTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTTGCAG GGGCACGCC AAATCTCCAG	120
GCATTGAGCG GGTTTATCCA AGAAAGGACC CGGTCGTCT GGCAATTCCG GTGTACTCAC	180
CGGTTCCGCA GACCACTATG GCTCTCCGG GAGGGGGGGT CCTGGAGGCT GCACGACACT	240
CATACTAACG CCATGGCCAG ACGCTTCTG CGTGAAGACA G	281

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 281 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAAGCACCC TATCAGGCAG TACCACAAGG	60
CCTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTTGCAG GGGCACGCC AAATCTCCAG	120
GCATTGAGCG GGTTGATCCA AGAAAGGACC CGGTCGTCT GGCAATTCCG GTGTACTCAC	180

CGGTTCCGCA GACCACTATG GCTCTCCGG GAGGGGGGGT CCTGGAGGCT GCACGACACT	240
CATACTAACG CCATGGCTAG ACGCTTTCTG CGTGAAGACA G	281

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 281 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAAGCACCC TATCAGGCAG TACCACAAGG	60
CCTTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTCGCGG GGGCACGCC AAATCTCCAG	120
GCATTGAGCG GGTTGATCCA AGAAAGGACC CGGTCGTCTT GGCAATTCCG GTGTACTCAC	180
CGGTTCCGCA GACCACTATG GCTCTCCGG GAGGGGGGGT CCTGGAGGCT GCACGACACT	240
CATACTAACG CCATGGCTAG ACGCTTTCTG CGTGAAGACA G	281

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 282 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAAGCACCC TATCAGGCAG TACCACAAGG	60
CCTTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTTGCAGG GGGCACGCC AAATCTCCAG	120
GCATTGAGCG GGTTACATCC ACGAAAGGAC CGGGTCGTCC TGGCAATTCC GGTGTACTCA	180
CCGGTTCCGC AGACCACTAT GGCTCTCCGG GGAGGGGGGG TCCTGGAGGC TGCACGACAC	240
TCATACTAAC GCCATGGCTA GACGCTTTCT GCGTGAAGAC AG	282

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 281 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GCACGGTCTA CGAGACCTCC CGGGGTACTC GCAAGCACCC TATCAGGCAG TACCACAAGG	60
CCTTTCGCAA CCCAACGCTA CTCGGCTAGC AGTCTTGCAG GGGCACGCCA AAATGGCCGG	120
GCATAGAGTG GGTTTATCCA AGAAAGGACC CAGTCTTCCC GGCAATTCCG GTGTACTCAC	180
CGGTTCCGCA GACCACTATG GCTCTCCCGG GAGGGGGGGG CCTGGAGGCT GTACGACACT	240
CATACTAACG CCATGGCTAG ACGCTTTCTG CGTGAAGACA G	281

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 281 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

GCACGGTCTA CGAGACCTCC CGGGGCACCTC GCAAGCACCC TATCAGGCAG TACCACAAGG	60
CCTTTCGCGA CCCAACACTA CTCGGCTAGT GATCTCGCGG GGGCACGCCA AAATTTCTGG	120
GTATTGAGCG GGTTGCTCCA AGAAAGGACC CGGTACCCCC AGCGATTCCG GTGTACTCAC	180
CGGTTCCGCA GACCACTATG GCTCTCCCGG GAGGGGGGGT CCTGGAGGCT GCACGACACT	240
CGTACTAACG CCATGGCTAG GCGCTTTCTG CGTGAAGACA G	281

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

ATCAACATCC GGCCGGTGGT	20
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(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GGGGCCTCGC TACGGACCAAG

20

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 620 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ATCAACATCC GGCGGTGGT CGCCGCGATC AAGGAGTTCT TCGGCACCAG CCAGCTGAGC	60
CAATTATGG ACCAGAACAA CCCGCTGTCG GGGTTGACCC ACAAGCGCCG ACTGTCGGCG	120
CTGGGGCCCG GCGGTCTGTC ACGTGAGCGT GCCGGGCTGG AGGTCCGCGA CGTGCACCCG	180
TCGCACTACG GCCGGATGTG CCCGATCGAA ACCCCTGAGG GGCCCAACAT CGGTCTGATC	240
GGCTCGCTGT CGGTGTACGC GCGGGTCAAC CCGTCGGGT TCATCGAAAC GCCGTACCGC	300
AAGGTGGTCG ACGGCGTGGT TAGCGACGAG ATCGTGTACC TGACCGCCGA CGAGGGAGGAC	360
CGCCACGTGG TGGCACAGGC CAATTGCGCG ATCGATGCGG ACGGTCGCTT CGTCGAGCCG	420
CGCGTGCTGG TCCGCCGCAA GGCGGGCGAG GTGGAGTACG TGCCCTGTC TGAGGTGGAC	480
TACATGGACG TCTCGCCCCG CCAGATGGTG TCGGTGGCCA CCGCGATGAT TCCCTTCCTG	540
GAGCACGACG ACGCCAACCG TGCCCTCATG GGGGCAAACA TGCAGCGCCA GGCGGTGCCG	600
CTGGTCCGTA GCGAGGCCCC	620

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 620 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

ATCAACATCC GGCGGTGGT CGCCGCGATC AAGGAGTTCT TCGGCACCAG CCAGCTGAGC	60
CAATTATGG ACCAGAACAA CCCGCTGTCG GGGTTGACCT ACAAGCGCCG ACTGTCGGCG	120
CTGGGGCCCG GCGGTCTGTC ACGTGAGCGT GCCGGGCTGG AGGTCCGCGA CGTGCACCCG	180
TCGCACTACG GCCGGATGTG CCCGATCGAA ACCCCTGAGG GGCCCAACAT CGGTCTGATC	240

GGCTCGCTGT CGGTGTACGC GCGGGTCAAC CCGTCGGGT TCATCGAAAC GCCGTACCGC	300
AAGGTGGTCTG ACGGCGTGGT TAGCGACGAG ATCGTGTACC TGACCGCCGA CGAGGAGGAC	360
CGCCACGTGG TGGCACAGGC CAATTGCGCG ATCGATGCGG ACGGTCGCTT CGTCGAGCCG	420
CGCGTGTGG TCCGCCGCAA GGCAGGCGAG GTGGAGTACG TGCCCTCGTC TGAGGTGGAC	480
TACATGGACG TCTCGCCCCG CCAGATGGTG TCGGTGGCCA CCGCGATGAT TCCCTTCCTG	540
GAGCACGACG ACGCCAACCG TGCCCTCATG GGGGCAAACA TGCAGGCCA GGCGGTGCCG	600
CTGGTCCGTA GCGAGGCCCC	620

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 620 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137

ATCAACATCC GGCCGGTGGT CGCCGCGATC AAGGAGTTCT TCGGCACCAG CCAGCTGAGC	60
CAATTCATGG ACCAGAACAA CCCGCTGTCG GGGTTGACCC ACAAGGCCG ACTGTTGGCG	120
CTGGGGCCCG GCGGTCTGTC ACGTGAGCGT GCGGGCTGG AGGTCCGCGA CGTGCACCCG	180
TCGCACTACG GCCGGATGTG CCCGATCGAA ACCCCTGAGG GGCCCAACAT CGGTCTGATC	240
GGCTCGCTGT CGGTGTACGC GCGGGTCAAC CCGTCGGGT TCATCGAAAC GCCGTACCGC	300
AAGGTGGTCTG ACGGCGTGGT TAGCGACGAG ATCGTGTACC TGACCGCCGA CGAGGAGGAC	360
CGCCACGTGG TGGCACAGGC CAATTGCGCG ATCGATGCGG ACGGTCGCTT CGTCGAGCCG	420
CGCGTGTGG TCCGCCGCAA GGCAGGCGAG GTGGAGTACG TGCCCTCGTC TGAGGTGGAC	480
TACATGGACG TCTCGCCCCG CCAGATGGTG TCGGTGGCCA CCGCGATGAT TCCCTTCCTG	540
GAGCACGACG ACGCCAACCG TGCCCTCATG GGGGCAAACA TGCAGGCCA GGCGGTGCCG	600
CTGGTCCGTA GCGAGGCCCC	620

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 620 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GGGGCCTCGC TACGGACCAG CGGCACCGCC TGGCGCTGCA TGTGCCCC CATGAGGGCA	60
CGGTTGGCGT CGTCGTGCTC CAGGAAGGGA ATCATCGCGG TGGCCACCGA CACCATCTGG	120
CGGGCGAGA CGTCCATGTA GTCCACCTCA GACGAGGGCA CGTACTCCAC CTCGCCCCGCC	180
TTGCGGCGGA CCAGCACGCG CGGCTCGACG AAGCGACCGT CCGCATCGAT CGGCGAATTG	240
GCCTGTGCCA CCACGTGGCG GTCCTCCTCG TCGGCGGTCA GGTACACGAT CTCGTCGCTA	300
ACCACGCCGT CGACCACCTT GCGGTACGGC GTTTCGATGA ACCCGAACGG GTTGACCCGC	360
GCGTACACCG ACAGCGAGCC GATCAGACCG ATGTTGGGCC CCTCAGGGGT TTCGATCGGG	420
CACATCCGGC CGTAGTGCAGA CGGGTGCACG TCGCGGACCT CCAGCCCCGC ACGCTCACGT	480
GACAGACCGC CGGGCCCCAG CGCCGACAGT CGGGCCTTGT GGGTCAACCC CGACAGCGGG	540
TTGTTCTGGT CCATGAATTG GCTCAGCTGG CTGGTGCCGA AGAACTCCTT GATCGCGGCG	600
ACCACCGGCC GGATGTTGAT	620

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGGGCCTCGC TACGGACCAG CGGCACCGCC TGGCGCTGCA TGTGCCCC CATGAGGGCA	60
CGGTTGGCGT CGTCGTGCTC CAGGAAGGGA ATCATCGCGG TGGCCACCGA CACCATCTGG	120
CGGGCGAGA CGTCCATGTA GTCCACCTCA GACGAGGGCA CGTACTCCAC CTCGCCCCGCC	180
TTGCGGCGGA CCAGCACGCG CGGCTCGACG AAGCGACCGT CCGCATCGAT CGGCGAATTG	240
GCCTGTGCCA CCACGTGGCG GTCCTCCTCG TCGGCGGTCA GGTACACGAT CTCGTCGCTA	300
ACCACGCCGT CGACCACCTT GCGGTACGGC GTTTCGATGA ACCCGAACGG GTTGACCCGC	360
GCGTACACCG ACAGCGAGCC GATCAGACCG ATGTTGGGCC CCTCAGGGGT TTCGATCGGG	420
CACATCCGGC CGTAGTGCAGA CGGGTGCACG TCGCGGACCT CCAGCCCCGC ACGCTCACGT	480
GACAGACCGC CGGGCCCCAG CGCCGACAGT CGGGCCTTGT AGGTCAACCC CGACAGCGGG	540
TTGTTCTGGT CCATGAATTG GCTCAGCTGG CTGGTGCCGA AGAACTCCTT GATCGCGGCG	600
ACCACCGGCC GGATGTTGAT	620

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 620 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GGGGCCTCGC TACGGACCAG CGGCACCGCC TGGCGCTGCA TGTGCGCCCC CATGAGGGCA	60
CGGTTGGCGT CGTCGTGCTC CAGGAAGGGA ATCATCGCG TGGCCACCGA CACCATCTGG	120
CGGGGCGAGA CGTCCATGTA GTCCACCTCA GACGAGGGCA CGTACTCCAC CTCGCCCCGCC	180
TTGCGGGCGGA CCAGCACGCG CGGCTCGACG AAGCGACCGT CCGCAGCGAT CGGCGAATTG	240
GCCTGTGCCA CCACGTGGCG GTCCTCCTCG TCGGCGGTCA GGTACACGAT CTCGTCGCTA	300
ACCACGCCGT CGACCACCTT GCGGTACGGC GTTTCGATGA ACCCGAACGG GTTGACCCGC	360
GCGTACACCG ACAGCGAGCC GATCAGACCG ATGTTGGGCC CCTCAGGGGT TTCGATCGGG	420
CACATCCGGC CGTAGTGGCA CGGGTGCACG TCGCGGACCT CCAGCCCCGC ACCGTCACGT	480
GACAGACCGC CGGGCCCCAG CGCCAACAGT CGGCAGCTTGT GGGTCAACCC CGACAGCGGG	540
TTGTTCTGGT CCATGAATTG GTCAGCTGG CTGGTGCCGA AGAACTCCTT GATCGCGCG	600
ACCACCGGCC GGATGTTGAT	620

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

AGCTCGTATG GCACCGGAAC	20
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(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

TTGACCTCCC ACCCGACTTG	20
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(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA CGGGCATCGA GGTCTATGG	60
ACGAACACCC CGACGAAATG GGACAACAGT TTCCTCGAGA TCCTGTACGG CTACGAGTGG	120
GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC	180
GGCACCATCC CGGACCCGTT CGGCGGGCCA GGGCGCTCCC CGACGATGCT GGCACTGAC	240
CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTCGCTGGCT GGAACACCCC	300
GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT	360
CCCGTTGCGA GATACCTTGG GCCGCTGGTC CCCAAGCAGA CCCTGCTGTG GCAGGGATCCG	420
GTCCCTGCGG TCAGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG	480
ATCCGGGCAT CGGGATTGAC TGTCTCACAG CTAGTTTCGA CCGCATGGC GGCGCGTCG	540
TCGTTCCGTG GTAGCGACAA GCGCGGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA	600
CAAGTCGGGT GGGAGGTCAA	620

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA CGGGCATCGA GGTCTATGG	60
ACGAACACCC CGACGAAATG GGACAACAGT TTCCTCGAGA TCCTGTACGG CTACGAGTGG	120
GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC	180
GGCACCATCC CGGACCCGTT CGGCGGGCCA GGGCGCTCCC CGACGATGCT GGCACTGAC	240
CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTCGCTGGCT GGAACACCCC	300
GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT	360
CCCGTTGCGA GATACCTTGG GCCGCTGGTC CCCAAGCAGA CCCTGCTGTG GCAGGGATCCG	420
GTCCCTGCGG TCAGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG	480

ATCCGGGCAT CGGGATTGAC TGTCTCACAG CTAGTTCGA CCGCATGGC GGCGCGTCG	540
TCGTTCCGTG GTAGCGACAA GCGCGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA	600
CAAGTCGGGT GGGAGGTCAA	620

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 620 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA CGGGCATCGA GGTCTATGG	60
ACGAACACCC CGACGAAATG GGACAACAGT TTCTCGAGA TCCTGTACGG CTACGAGTGG	120
GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC	180
GGCACCATCC CGGACCCGTT CGGCGGGCCA GGGCGCTCCC CGACGATGCT GGCCACTGAC	240
CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTCGCTGGCT GGAACACCCC	300
GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT	360
CCCGTTGCCA GATACTTG GCGCTGGTC CCCAAGCAGA CCCTGCTGTG GCAGGATCCG	420
GTCCCTGCGG TCAGGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG	480
ATCCTGGCAT CGGGATTGAC TGTCTCACAG CTAGTTCGA CCGCATGGC GGCGCGTCG	540
TCGTTCCGTG GTAGCGACAA GCGCGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA	600
CAAGTCGGGT GGGAGGTCAA	620

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 620 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA CGGGCATCGA GGTCTATGG	60
ACGAACACCC CGACGAAATG GGACAACAGT TTCTCGAGA TCCTGTACGG CTACGAGTGG	120
GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC	180
GGCACCATCC CGGACCCGTT CGGCGGGCCA GGGCGCTCCC CGACGATGCT GGCCACTGAC	240
CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTCGCTGGCT GGAACACCCC	300

GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT	360
CCCGTTGCGA GATACCTTGG GCCGCTGGTC CCCAAGCAGA CCCTGCTGTG GCAGGGATCCG	420
GTCCCTGCGG TCAGGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG	480
ATCCTGGCAT CGGGATTGAC TGTCTCACAG CTAGTTCGA CCGCATGGC GGCGCGTCG	540
TCGTTCCGTG GTAGCGACAA GCGCGGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA	600
CAAGTCGGGT GGGAGGTCAA	620

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 620 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

TTGACCTCCC ACCCGACTTG TGGCTGCAGG CGGATGCGAC CACCGTTGGC GCCGCCGCGC	60
TTGTCGCTAC CACGGAACGA CGACGCCGCC GCCCATGCGG TCGAAACTAG CTGTGAGACA	120
GTCAATCCCC ATGCCCGGAT CTGGCTCTTA AGGCTGGCAA TCTCGGCTTC GCCGACGAGG	180
TCGTGGCTGA CCGCAGGGAC CGGATCCTGC CACAGCAGGG TCTGTTGGG GACCAGCGGC	240
CCAAGGTATC TCGCAACGGG ACCCATGTCT CGGTGGATCA GCTTGTACCA GGCTTGGCG	300
AACTCGTCGG CCAATTCCCTC GGGGTGTTCC AGCCAGCGAC GCGTGATCCG CTCATAGATC	360
GGATCCACCC GCAGCGAGAG GTCAGTGGCC AGCATCGTCG GGGAGCGCCC TGGCCCGCCG	420
AACGGGTCCG GGATGGTGCC GGCACCGGGCG CCGTCCTTGG CGGTGTATTG CCAAGCGCCA	480
GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CCGTACAGGA TCTCGAGGAA ACTGTTGTCC	540
CATTCGTGCG GGGTGTTCGT CCATACGACC TCGATGCCGC TGGTGATCGC GTCCTTACCG	600
GTTCCGGTGC CATAcgagct	620

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 620 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

TTGACCTCCC ACCCGACTTG TGGCTGCAGG CGGATGCGAC CACCGTTGGC GCCGCCGCGC	60
TTGTCGCTAC CACGGAACGA CGACGCCGCC GCCCATGCGG TCGAAACTAG CTGTGAGACA	120

GTCAATCCCG ATGCCCGGAT CTGGCTCTTA AGGCTGGCAA TCTCGGCTTC GCCGACGAGG	180
TCGTGGCTGA CGCGAGGGAC CGGATCCTGC CACAGCAGGG TCTGCTTGGG GACCAGCGGC	240
CCAAGGTATC TCGCAACGGG ACCCATGTCT CGGTGGATCA GCTTGTACCA GGCCTTGGCG	300
AACTCGTCGG CCAATTCTC GGGGTGTTCC AGCCAGCGAC GCGTGATCCG CTCATAGATC	360
GGATCCACCC GCAGCGAGAG GTCAGTGGCC AGCATCGTCG GGGAGCGCCC TGGCCCGCCG	420
AACGGGTCCG GGATGGTGCC GGCACCGGCG CCGTCCTTGG CGGTGTATTG CCAAGCGCCA	480
GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CCGTACAGGA TCTCGAGGAA ACTGTTGTCC	540
CATTTCGTCG GGGTGTTCGT CCATACGACC TCGATGCCGG TGGTGATCGC GTCCTTACCG	600
GTTCCGGTGC CATACTGAGCT	620

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 620 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

TTGACCTCCC ACCCGACTTG TGGCTGCAGG CGGATGCGAC CACCGTTGGC GCCGCCGCGC	60
TTGTCGCTAC CACGGAACGA CGACGCCGCC GCCCATGCGG TCGAAACTAG CTGTGAGACA	120
GTCAATCCCG ATGCCAGGAT CTGGCTCTTA AGGCTGGCAA TCTCGGCTTC GCCGACGAGG	180
TCGTGGCTGA CGCGAGGGAC CGGATCCTGC CACAGCAGGG TCTGCTTGGG GACCAGCGGC	240
CCAAGGTATC TCGCAACGGG ACCCATGTCT CGGTGGATCA GCTTGTACCA GGCCTTGGCG	300
AACTCGTCGG CCAATTCTC GGGGTGTTCC AGCCAGCGAC GCGTGATCCG CTCATAGATC	360
GGATCCACCC GCAGCGAGAG GTCAGTGGCC AGCATCGTCG GGGAGCGCCC TGGCCCGCCG	420
AACGGGTCCG GGATGGTGCC GGCACCGGCG CCGTCCTTGG CGGTGTATTG CCAAGCGCCA	480
GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CCGTACAGGA TCTCGAGGAA ACTGTTGTCC	540
CATTTCGTCG GGGTGTTCGT CCATACGACC TCGATGCCGG TGGTGATCGC GTCCTTACCG	600
GTTCCGGTGC CATACTGAGCT	620

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 620 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

TTGACCTCCC ACCCGACTTG TGGCTGCAGG CGGATGCGAC CACCGTTGGC GCCGCCGCGC	60
TTGTCGCTAC CACGGAACGA CGACGCCGCC GCCCATGCGG TCGAAACTAG CTGTGAGACA	120
GTCAATCCCG ATGCCAGGAT CTGGCTCTTA AGGCTGGCAA TCTCGGCTTC GCCGACGAGG	180
TCGTGGCTGA CCGCAGGGAC CGGATCCTGC CACAGCAGGG TCTGCTTGGG GACCAGCGGC	240
CCAAGGTATC TCGCAACGGG ACCCATGTCT CGGTGGATCA GCTTGTACCA GCCCTTGGCG	300
AACTCGTCGG CCAATTCCCTC GGGGTGTTCC AGCCAGCGAC GCGTGATCCG CTCATAGATC	360
GGATCCACCC GCAGCGAGAG GTCAGTGGCC AGCATCGTCG GGGAGCGCCC TGGCCCGCCG	420
AACGGGTCCG GGATGGTGCC GGCACCGGGCG CCGTCCTTGG CGGTGTATTG CCAAGCGCCA	480
GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CCGTACAGGA TCTCGAGGAA ACTGTTGTCC	540
CATTCGTCG GGGTGTTCGT CCATACGACC TCGATGCCGG TGGTGATCGC GTCCTTACCG	600
GTTCCGGTGC CATACTGAGCT	620

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

AGAGTTTGAT CCTGGCTCAG	20
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(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GGCGGACGGG TGAGTAA	17
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(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:  
CTGCTGCCTC CCGTAGGAGT 20

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:  
ATGACGTCAA GTCATCATGG CCCTTACGA 29

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:  
GTACAAGGCC CGGGAACGTA TTCACCG 27

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:  
GCAACGAGCG CAACCC 16

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:  
ATGACGTCAA GTCATCATGG CCCTTA 26

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

AAATTGAAGA	60
GTTTGATCAT	
GGCTCAGATT	
GAACGCTGGC	
GGCAGGCCTA	
ACACATGCAA	
GTCGAACGGT	120
AACAGGAAGA	
AGCTTGCTTC	
TTTGCTGACG	
AGTGGCGGAC	
GGGTGAGTAA	
TGTCTGGGAA	180
ACTGCCTGAT	
GGAGGGGGAT	
AACTACTGGA	
AACGGTAGCT	
AATACCGCAT	
AACGTCGCAA	240
GACCAAAGAG	
GGGGACCTTC	
GGGCCTCTT	
CCATCGGATG	
TGCCAGATG	
GGATTAGCTA	300
GTAGGTGGGG	
TAACGGCTCA	
CCTAGGCGAC	
GATCCCTAGC	
TGGTCTGAGA	
GGATGACCAG	360
CCACACTGGA	
ACTGAGACAC	
GGTCAGACT	
CCTACGGGAG	
GCAGCAGTGG	
GGAATATTGC	420
ACAATGGCG	
CAAGCCTGAT	
GCAGCCATGC	
CGCGTGTATG	
AAGAAGGCCT	
TCGGGTTGTA	480
AACTACTTTC	
AGCGGGGAGG	
AAGGGAGTAA	
AGTTAATACC	
TTTGCTCATT	
GACGTTACCC	540
GCAGAAGAAG	
CACCGGCTAA	
CTCCGTGCCA	
GCAGCCGCGG	
TAATACGGAG	
GGTGCAAGCG	600
TTAACCGGAA	
TTACTGGCG	
TAAAGCGCAC	
GCAGGCGGTT	
TGTTAAGTCA	
GATGTGAAAT	660
CCCCGGGCTC	
AACCTGGAA	
CTGCATCTGA	
TACTGGCAAG	
CTTGAGTCTC	
GTAGAGGGGG	720
GTAGAATTCC	
AGGTGTAGCG	
GTGAAATGCG	
TAGAGATCTG	
GAGGAATACC	
GGTGGCGAAG	780
GGGGCCCCCT	
GGACGAAGAC	
TGACGCTCAG	
GTGCGAAAGC	
GTGGGGAGCA	
AACAGGATTA	840
GATACCCTGG	
TAGTCCACGC	
CGTAAACGAT	
GTGCACTTGG	
AGGTTGTGCC	
CTTGAGGCGT	900
GGCTTCCGGA	
GCTAACGCGT	
TAAGTCGACC	
GCCTGGGGAG	
TACGGCCGCA	
AGGTTAAAAC	960
TCAAATGAAT	
TGACGGGGC	
CCGCACAAGC	
GGTGGAGCAT	
GTGGTTAAC	
TCGATGCAAC	1020
GCGAAGAAC	
TTACCTGGTC	
TTGACATCCA	
CGGAAGTTTT	
CAGAGATGAG	
AATGTGCCTT	1080
CGGGAACCGT	
GAGACAGGTG	
CTGCATGGCT	
GTGTCAGCT	
CGTGTGTGA	
AATGTTGGGT	1140
TAAGTCCCGC	
AACGAGCGCA	
ACCCTTATCC	
TTTGTGCCA	
CGGGTCCGGC	
CGGGAACTCA	1200
AAGGAGACTG	
CCAGTGATAA	
ACTGGAGGAA	
GGTGGGGATG	
ACGTCAAGTC	
ATCATGGCCC	1260
TTACGACCAG	
GGCTACACAC	
GTGCTACAAT	
GGCGCATACA	
AAGAGAAGCG	
ACCTCGCGAG	1320
AGCAAGCGGA	
CCTCATAAAG	
TGCGTCGTAG	
TCCGGATTGG	
AGTCTGCAAC	
TCGACTCCAT	1380
GAAGTCGGAA	
TCGCTAGTAA	
TCGTGGATCA	
GAATGCCACG	
GTGAATACTGT	

TCCCGGGCCT	TGTACACACC	GCCCCTCACA	CCATGGGAGT	GGGTTGCAAA	AGAAGTAGGT	1440
AGCTTAACCT	TCGGGAGGGC	GCTTACCACT	TTGTGATTCA	TGACTGGGGT	GAAGTCGTAA	1500
CAAGGTAACC	GTAGGGGAAC	CTGCGGTTGG	ATCACCTCCT	TA		1542

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1513 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

TTTTTATGGA	GAGTTGATC	CTGGCTCAGA	GTGAACGCTG	GCGGCGTGCC	TAATACATGC	60
AAGTCGAACG	ATGAAGCTTC	TAGCTTGCTA	GAAGTGGATT	AGTGGCGCAC	GGGTGAGTAA	120
GGTATAGTTA	ATCTGCCCTA	CACAAGAGGA	CAACAGTTGG	AAACGACTGC	TAATACTCTA	180
TACTCCTGCT	TAACACAAGT	TGAGTAGGGA	AAGTTTTCG	GTGTAGGATG	AGACTATATA	240
GTATCAGCTA	GTTGGTAAGG	TAATGGCTTA	CCAAGGCTAT	GACGCTTAAC	TGGTCTGAGA	300
GGATGATCAG	TCACACTGGA	ACTGAGACAC	GGTCCAGACT	CCTACGGGAG	GCAGCAGTAG	360
GGAATATTGC	GCAATGGGGG	AAACCCTGAC	GCAGCAACGC	CGCGTGGAGG	ATGACACTTT	420
TCGGAGCGTA	AACTCCTTT	CTTAGGGAAG	AATTCTGACG	GTACCTAAGG	AATAAGCACC	480
GGCTAACTCC	GTGCCAGCAG	CCGCGGTAAT	ACGGAGGGTG	CAAGCGTTAC	TCGGAATCAC	540
TGGGCGTAAA	GGGCGCGTAG	GGGGATTATC	AAGTCTTTG	TGAAATCTAA	TGGCTTAACC	600
ATTAAACTGC	TTGGGAAACT	GATAGTCTAG	AGTGAGGGAG	AGGCAGATGG	AATTGGTGGT	660
GTAGGGGTAA	AATCCGTAGA	TATCACCAAG	AATACCCATT	GCGAAGGCAGA	TCTGCTGGAA	720
CTCAACTGAC	GCTAAGGCGC	GAAAGCGTGG	GGAGCAAACA	GGATTAGATA	CCCTGGTAGT	780
CCACGCCCTA	AACGATGTAC	ACTAGTTGTT	GGGGTGCTAG	TCATCTCAGT	AATGCAGCTA	840
ACGCATTAAG	TGTACCGCCT	GGGGAGTACG	GTCGCAAGAT	TAAAACCTCAA	AGGAATAGAC	900
GGGGACCCGC	ACAAGCGGTG	GAGCATGTGG	TTTAATTGCA	AGATACGCGA	AGAACCTTAC	960
CTGGGCTTGA	TATCCTAAGA	ACCTTTAGA	GATAAGAGGG	TGCTAGCTTG	CTAGAACTTA	1020
GAGACAGGTG	CTGCACGGCT	GTCGTCAGCT	CGTGTGCGA	GATGTTGGGT	TAAGTCCCGC	1080
AACGAGCGCA	ACCCACGTAT	TTAGTTGCTA	ACGGTTCGGC	CGAGCACTCT	AAATAGACTG	1140
CCTTCGTAAG	GAGGAGGAAG	GTGTGGACGA	CGTCAAGTCA	TCATGGCCCT	TATGCCAGG	1200
GCGACACACG	TGCTACAATG	GCATATAGAA	TGAGACGCAA	TACCGCGAGG	TGGAGCAAAT	1260
CTATAAAATA	TGTCCCAAGTT	CGGATTGTTG	TCTGCAACTC	GAGAGCATGA	AGCCGGAATC	1320

GCTAGTAATC GTAGATCAGC CATGCTACGG TGAATACGTT CCCGGGTCTT GTACTCACCG	1380
CCCGTCACAC CATGGGAGTT GATTCACTC GAAGCCGGAA TACTAAACTA GTTACCGTCC	1440
ACAGTGGAAAT CAGCGACTGG GGTGAAGTCG TAACAAGGTA ACCGTAGGAG AACCTGCGGT	1500
TGGATCACCT CCT	1513

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1555 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

TTTTATGGAG AGTTTGATCC TGGCTCAGGA TGAACGCTGG CGGCGTGCTT AATACATGCA	60
AGTCGAGCGA ACGGACGAGA AGCTTGCTTC TCTGATGTTA GCGGCGGACG GGTGAGTAAC	120
ACGTGGATAA CCTACCTATA AGACTGGGAT AACTTCGGGA AACCGGAGCT AATACCGGAT	180
AATATTTGA ACCGCATGGT TCAAAAGTGA AAGACGGTCT TGCTGTCACT TATAGATGGA	240
TCCGCGCTGC ATTAGCTAGT TGGTAAGGTA ACGGCTTACC AAGGCAACGA TACGTAGCCG	300
ACCTGAGAGG GTGATCGGCC ACACTGGAAC TGAGACACGG TCCAGACTCC TACGGGAGGC	360
AGCAGTAGGG AATCTTCCGC AATGGGCGAA AGCCTGACGG AGCAACGCCG CGTGAGTGAT	420
GAAGGTCTTC GGATCGTAAA ACTCTGTTAT TAGGGAAGAA CATATGTGTA AGTAACGTG	480
CACATCTTGA CGGTACCTAA TCAGAAAGCC ACGGCTAACT ACGTGCCAGC AGCCGCGGT	540
ATACGTAGGT GGCAAGCGTT ATCCGGAATT ATTGGCGTA AAGCGCGGT AGGCGGTTTT	600
TTAAGTCTGA TGTGAAAGCC CACGGCTCAA CCGTGGAGGG TCATTGGAAA CTGGAAAAGT	660
TGAGTGCAGA AGAGGAAAGT GGAATTCCAT GTGTAGCGGT GAAATGCCA GAGATATGGA	720
GGAACACCAAG TGGCGAAGGC GACTTTCTGG TCTGTAACG ACGCTGATGT GCGAAAGCGT	780
GGGGATCAAA CAGGATTAGA TACCTGGTA GTCCACGCCG TAAACGATGA GTGCTAAGTG	840
TTAGGGGGTT TCCGCCCTT AGTGTGCAAG CTAACGCATT AAGCACTCCG CCTGGGGAGT	900
ACGACCGCAA GGTTGAAACT CAAAGGAATT GACGGGGACC CGCACAAAGCG GTGGAGCATG	960
TGGTTAATT CGAAGCAACG CGAAGAACCT TACCAAATCT TGACATCCTT TGACAACCTCT	1020
AGAGATAGAG CCTTCCCTT CGGGGGACAA AGTGACAGGT GGTGCATGGT TGTCGTCAGC	1080
TCGTGTCGTG AGATGTTGGG TTAAGTCCCG CAACGAGCGC AACCCCTAAG CTTAGTTGCC	1140
ATCATTAAGT TGGGCACTCT AAGTTGACTG CCGGTGACAA ACCGGAGGAA GGTGGGGATG	1200
ACGTCAAATC ATCATGCCCT TTATGATTG GGCTACACAC GTGCTACAAT GGACAATACA	1260

AAGGGCAGCG AAACCGCGAG GTCAAGAAA TCCCATAAAG TTGTTCTCAG TTGGGATTGT	1320
AGTCTGCAAC TCGACTACAT GAAGCTGGAA TCGCTAGTAA TCGTAGATCA GCATGCTACG	1380
GTGAATACTGT TCCCGGGTAT TGTACACACC GCCCGTCACA CCACGAGAGT TTGTAACACC	1440
CGAAGCCGGT GGAGTAACCT TTTAGGAGCT AGCCGTCGAA GGTGGGACAA ATGATTGGGG	1500
TGAAGTCGTA ACAAGGTAGC CGTATCGGAA GGTGCGGCTG GATCACCTCC TTTCT	1555

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 46 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

GAAUACUCAA GCUUGCAUGC CUGCAGGUUC ACUCUAGAGG AUCCCC	46
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(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 141 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

TTGACAATTA ATCATCGGCT CGTATAATGT GTGGAATTGT GAGCGGATAA CAATTCACA	60
CAGGAAACAG CGATGAATTG GAGCTCGGTA CCCGGGGATC CTCTAGAGTC GACCTGCAGG	120
CATGCAAGCT TGGCACTGGC C	141

(2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 144 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

AGATCTCGAT CCCCGCAAAT TAATACGACT CACTATAGGG AGACCACAAAC GGTTCCCTC	60
TAGAAATAAT TTTGTTAAC TTTAAGAAGG AGATATAACAT ATGGCTAGCA TGACTGGTGG	120
ACAGCAAATG GGTGGATCC GGCT	144

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

TAATACGACT CACTATAGGG AGACCGGAAT TCGAATTCCG TGTATTCTAT AGTGTACCT	60
AAATCGAATT C	71

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

CGCCAGGGTT TTCCCAAGTCA CGACGTTGTA AAACGACGGC CAGTGAATTG TAATACGACT	60
CACTATAGGG CGAATTCGAG CTCGGTACCC GGGGATCCTC TAGAGTCGAC CTGCAGGCAT	120
GCAAGCTTGA GTATTCTATA GTGTCACCTA AATAGCTTGG CGTAATCATG GTCATAGCTG	180
TTTCCTGTGT GAAATTGTTA TCCGCTCACACA ATTCCACACACA ACATACGA	228